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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07-16-02 1949; MasPar time 9 OR Seconds 422.695 Million cell updates/sec Pur on.

Tabular output not generated.

>US-08-844-215-7 (1-125) from US09844215 pep 949

1 EVQLLESGSEVKKPGSSVKV Description: Perfect Score: Sedneuce.

GSCWGWFDPWGQGTLVTVSS 126

PAM 150 Gap 11 Scoring table:

95051 seqs, 30469580 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

Transl 2.ans2 3 ans3 4.ars4 5 state; 6 unios2 7:state; 8 sunant4 9.unant5 10.unant6 11.unant7 12.unant8 18.unant9 14:unant10 15:unant11 16:unant12 17:unenc

Mean 40,893; Variance 107.589; scale 0.380 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. SC	Score	Query Match	Query Match Length	DB	ID	Description	D.	Pred. No.
	ın	79.5	7	7	CD.	Ig heavy	chain V reg	9e-9
	~	70.7	128	~	S	Ig heavy	chain V reg	2e-8
	9	69.7	7	7	A33548	Ig heavy	chain V-1 r	6e-8
	657	69.2	116	۲	PH0959	Ig heavy	chain V req	6.97e-81
	4	80	C+	۲-	856083	i tr	thain V red	50.7
	Ť	68.1	120	7	PH0962	Id heavy	chain V red	7
	4	۲.	7	7	B33548	Iq heavy	chain V-1 r	9e-7
	4	67.7	~	7	PH0955	Iq heavy	chain V req	9e-7
	3	7	۴.	7	PH0954	ь	chain V req	F-9
	3	67.2	119	7	PH0961	Id heavy	chain V red	.246-7
	3	9	7	۲-	A49590	Ig heavy	chain V req	616-7
	3	66.7	\sim	7	PH0953	6	in V r	.72e-7
	3	ġ.	133	7	C33548	Iq heavy	chain V-1 r	.32e-7
	3	ç.	\sim	7	S14683	Iq mu cha	in precurso	.32e-7
	\sim	9	98	7	S26915	Iq heavy	chain V req	.55e-7
	\sim	9	Н	^	S31698	Iq heavy	chain precu	.55e-7
	α	9	123	7	S44108	b	chain V-D-J	.55e-7
	C1	66.2	-1	۲.	836261	ь	chain V req	20-7
	~	9	86	7	2468	Iq heavy	chain V1 re	3.17e-76
	CI	65.5	136	۲-	PH0960	Ig heavy	chain V reg	9e-7

3.86e-75 5.51e-75 1.61e-74	.85e-7	.18e-7	.18e-7 .97e-7	.42e-6	.130-6	.20e-6	.01e-6	.94e-6	.94e-6	.01e-6	.05e-6	.93e-6	.17e-5	.94e-6	01e-6	.43e-5	.19e-6	.19e-6	.70e-6	450-6
Ig heavy chain V reg Ig heavy chain V-D-J Ig heavy chain V reg	g heavy chain	g heavy chain	თ ი	g heavy chain	nti-PR2 erythr	g heavy chain	g heary chain													
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11 C1 C1	C1 C	52	C1 C1	59	30	31	32	33	34	35	36	37	æ €	39	C)	4.1	42	43	44	4 E

ALIGNMENTS

ENTRY TITLE ORGANISM DATE ACCESSIONS	PH0957 #type fragment Ig heavy chain V region (G6+ CLL-BRA) - human (fragment) #formal_name Homo sapiens #common_name man 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
#2012hrs	Martin, I., buffy, S.F., Carson, D.A., Ripps, T.G.
#journal	75:983-991
#title #cross-refere	#title Evidence for somatic selection of natural autoantibodies.
#accession	CGS MCID: 31101000
##status	nucleic acid sequence not shown
##molecule_type DNA	type DNA
##residues	25 ##label MAR
KEYWORDS	*Superiamily immunoglobulin v region; immunoglobulin nomology heterotetramer: immunoglobulin
FEATURE	
1-30	#region framework 1\
15-98	
31-35	
36-50	framework 2\
51-67	-
58-98	tramework 3/
99-II3 SUMMARY	#region complementarity-determining 3 #length 125 #checksum 8143
* · · · · · · · · · · · · · · · · · · ·	
Best Local Similarity Matches 107; Conser	83 6%; Pred No 4.99e-96; vative 9; Mismatches 7
1 qvq1vq	gayalıyasaevkkpasvkysckaegetissyalnwirgapagalewagalipifgtany 60
Oy 1 EVQLLE	SGSEVKKPGSSVKVSCPASGGSFPSYNFNWVRQAPGQGLEWMGGIIPMFGTANY 60
Db 61 aqkfqg	rvtitadestntaymelsslrsedtavyycard-gcsggscyfwgwfdpwgg 117
QY 61 AQKFQG	AQKFQGRVT1TADESTATGYMELSSLRSEDTAVYYCAMPYPKHCSRGSCWGWFDPWGQ 118
Db 118 gtlytyss	ss 125
Qy 119 GILVIVSS	 SS 126

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#superfamily immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kipps, T.J.; Tomhave, E., Pratt, L.F.; Duffy, S., Chen, P.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc Natl Acad Sci U.S.A. (1989, 86.5913-5917
Developmentally restricted immunoglobulin heavy chain
variable region gene expressed at high frequency in chroniv-
lymphocytic leukemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 aqkfqarvtitadkststaymelsslrsed†avyycarggnydyiwgsyrsndafdiwgg 120 \,
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                  PH0952 *type fragment | 1g heavy chain V region (66+ CLL-SMI) - human (fragment) | #formal_name Homo sapiens #common_name man | 17-Apr-1993 *sequence_revision 17-Apr-1993 *text_change
                                                                                                                                                                           *authors Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
#tille Evidence for somatic selection of natural autoantibodies
#cross-references MUID:92202880
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J. Exp. Med. (1992) 175:983-991
Evidence for somatic selection of natural autoantibodies.
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IghBeay_chain_v1_region_(NEI) - human
Heavy_chain_v2_region_tongre_man
Hermal_name_Homo_sapiens_tcommon_name_man
17.Jan-1990_#sequence_revision_17-Jan-1990_#text_change
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#region complementarity-determining 2\
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*region complementarity-determining 3
*length 128 *checksum 3537
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Pred. No. 4.62e-83;
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Matches 97; Conservative
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99-116
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36-50
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RESULT
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1-129 ##label MAR
#superfamily immunoglobulin V region; immunoglobulin homolody
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                                                                                                                                                                                                                                                                                                                  #authors Martin, I.; Duffy, S.F.; Carson, D.A.; Kipps, T.J., #fourmal J. Exp. Med. (1992) 175:983-991
#tille Evidence for somatic selection of natural autoantibodies.
#cross_references_MUID:92202880
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#length 129 #molecular-weight 13932 #checksum 3075
                                                                                           immynoglobylin homology #label IMMV
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                                                                                           #domain immunoglobulin homolody #labol
#region complementarity-determinind l\
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#region complementarity-determining 2\
#region framework 3\
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#region complementarity-determining 2\
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                                                                                                                                                                                                                                        Score 661; DB 7;
Pred. No. 1.66e-81;
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Best Local Similarity 80.2%; Pred. No. 6.97e-81;
Matches 101; Conservative 11; Mismatches 4
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Local Similarity 76.9%;
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                 CLASSIFICATION
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STIMMAPY
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99:104
SUMMARY
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ORGANISM
                                     KEYWORDS
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#journal J. Exp. Med. (1992) 175:983-991
Exp. Med. (1992) 175:983-991
Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MuID:92202880
#accession PH0958
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#fournal J. Exp. Med. (1992) 175:983-991
#title Evidence for sometic selection of natural autoantibodies.
#cross-references MUID:92202880
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Proc Natl Acad Sci U S A (1989) 86:5913-5917

Developmentally restricted immunoglobulin heavy chain variable region gene expressed at high frequency in lymphocytic leukemia.
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Query Match 68.1%; Score 646; DB 7; 1
Best Local Similarity 77.8%; Pred. No. 3.57e-79;
Matches 98; Conservative 13; Mismatches 9.
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Best Local Similarity 74.6%; Pred. No. 1.49e-78;
Matches 94; Conservative 12; Mismatches 20,
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#title Evidence for somatic selection of natural autoantibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 642; DB 7; Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 4.37e-78;
16; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                      #region complementarity-determining 2\
#region framework 3\
#region complementarity-determining 3
#length 127 #checksum 6297
                                                                                                                                                                                                                                                                                         #region complementarity-determining 1\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #region complementarity-determining 1/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #region complementarity-determining 2\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #region complementarity-determining 3
#length 132 #checksum 9232
                                                                                                   nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.49e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 7;
                                                                                                                                                                                               heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 639;
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                                                                                                                                                -127 ##label MAR
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#accession PH0954
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 74.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 72.7%;
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 38;
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                                                                                                                          ##molecule_type DNA
##residues 1-13
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SUMMARY
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FEATURE
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FEATURE
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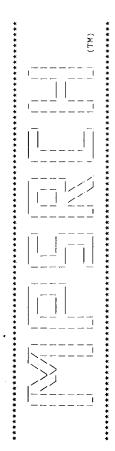
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A49590 #type fragment
Igh beavy chain V region (ACHSV1, clone 15) - human (fragment)
Meavy chain V sepiens #common_name man
06-oct-1994 #sequence_revision 18-Nov-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *superfamily immancylobulin V region: immunoglobulin homology
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##note sequence extracted from NCBI backbone
##note ##
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##status preliminary, not compared with conceptual translation ##molecule_type nucleic acid
61 AUKFUGRVIITADESTATGYMELSSLRSEDTAVYYCAMPYPK-HCSRGSCW-GWF----D 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #title Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 qvqlvqsgaevkkpgssvkvsckasggtfssyaiswvrqapgqqlewmqgiipifqtany 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burioni, R.; Williamson, R.A.; Sanna, P.P.; Bloom, F.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #title Recombinant human Fab to glycoprotein D neutralizes infectivity and prevents cell-to-cell transmission of herpes simplex viruses 1 and 2 in vitro. #accession A49590 #status
                                                                                                                                                                                                                                                                                                                                                                                                                   #formal_name Homo sapiens #common_name man
17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
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                                                                                                                                                                                                                                                                                                                                     PH0961 #type fragment
Ig heavy chain V region (G6+ T-L33) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J. J. Exp Med. (1992) 175:983-991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #domain immunoglobulin homology #label IMM\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
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#region complementarity-determining 3
#Jength 119 #checksum 9601
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34-117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *superfamily immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                     61 ggrvtftadaststaymelsslrsedtavyycarv-g-ycstngcslggmdvwgggttvi 118
                                                                                                                                                                                                                                                       65 QGRVIITADESTATGYMELSSLRSEDTAVYYCAMPYPKHCSRGSCW-GWFDPWGQGTLVT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                  PH0953 *type fragment if howary chain V region (68-02LL-SI2) - human (fragment) *formal_name Homo sapiens *common_name man 17-Apr-1993 *sequence_revision 17-Apr-1993 *text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #authors Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J Exp Med. (1992) 175-983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
                                                                                                                                                        1 lesgaevkkpgssvkvscktsggafssyainwvrqapggglewmggilpvfgttnhaqkf 60
                                                                                                                                                                                             5 LESGSEVKKPGSSVKVSCRASGGSFRSYNFNWVRQAPGQGLEWMGGIIPMFGTANYAQKF 64
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Igh heavy chain V-1 region (783) - human
Americanal_name Homo sapiens *common_name man
17.Jan-1990 *sequence_revision 17.Jan-1990 *text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #domain immunoglobulin homology #label IMM\
                  #domain immunoglobulin homology #label 1MM
#length 121 #checksum 6226
                                                                          Score 634; DB 7; Length 121; Pred No. 2.610-77; 12; Mismatches 16; Indels
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#region complementarity-determining 2\
#region framework 3\
#region complementarity-determining 3
#length 135 #checksum 2318
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                                                                            Query Match 66.8%;
Best Local Similarity 74 8%;
Matches 92; Conservative
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##experimental_source the sequence was determined from the differentiated gene differantlated gene FICATION #superfamily immunoglobulin V region; immunoglobulin homology to heterotetramer; immunoglobulin
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CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
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*product Ig mu chain *status predicted *label MAT\
#domain immunoglobulin homology *label IMM
#length 627 *molecular weight 68510 *checksum 8581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *authors Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
#journal Nucleic Acids Res (1940) 18:4278
#title Complete nucleotide sequence of the membrane form of the human 19M heavy chain.
#cross-references MUID:90332450
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Pred. No. 5.32e-77;
15; Mismatches 14; Indels 7; Gaps
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Best Local Similarity 72.9%; Fred. No. 5.32e-77;
Matches 97, Conservative 15, Mismatches 14, Indels 7, Gaps
                                                                                                                                                        preliminary; nucleic acid sequence not shown; not compared with conceptual translation
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##residues 1-627 ##label FRI
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Best Local Similarity 72.9%;
Matches 97; Conservative
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Winter, G.
J. Mol. Biol. (1992) 227:776-798
The repertoire of human germline V(H) sequences reveals about fifty groups of V(H) segments with different hypervariable loops.
S26915
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CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
                                                                       $26915  #type fragment | human (fragment) | heavy chain V region (DP-10) - human (fragment) | #formal_name Homo sapiens #common_name man | 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997 | $26915 | Comlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 66.3%; Score 629; DB 7; Length 98; Best Local Similarity 86.6%; Pred. No. 1.55e-76; Matches 84; Conservative 11; Mismatches 2; Indels 0; Gaps
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##residue=
114 DPWGQGTLVTVSS 126
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#title
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ENTRY
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tue Feb 24 07:42:43 1999; MasPar time 3.28 Seconds 198.669 Million cell updates/sec Pun on.

Tabular output not generated.

Description: Perfect Score:

>US-08-844-215-7 (1-126) from US08844215 pep 949 1 EVQLLESGSEVKKPGSSVKV Sequence:

GSCWGWFDPWGQGTLVTVSS 126

PAM 150 Gap 11 Scoring table:

56402 seqs, 5095871 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued l:backl 2.51 3.52 4.53 5.54 6.55 7.56 8.PCT90 9.PCT91 l0:PCT92 11.PCT93 12.PCT94 13:PCT95 14.PCT96 Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 28.440; Variance 143 456; scale 0 198 Statistics:

SUMMARIES

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Result No.	Score	Query	Length	DB	ID	Description	Pred. No.
1	635	6.99	120 1	: 1	PCT-US93-1	Sequence 13, Applicati	1.04e-42
7	609	64.2	120	딤	PCT-US93-1	C)	1.486-40
3	605	63.8	129	13	PCT-US95-0	45,	۴,
4	604	63.6	147	9	US-08-217-	4	3.85e-40
S	595	62.7	101	10	PCT-US92-0	Sequence 55, Applicati	2 146-39
9	595	62.7	10	۲	US-08-053-	63	2.14e-39
7	595	62 7	100	Ç.	FCT - US92 - 1	۲,	c.
8	565	62.7		۲	US-07-834-	55,	2.14
6	591	62.3		7	US-08-474-	15,	7
10	591	62.3		ç	US-08-477-	104,	4.58e-39
11	591	62.3		9	US-08-477-	4	4
12	591	62.3		9	US-08-477-	15	4.58e-39
13	591	62.3	117	(c)	US-08-477-	Sequence 72, Applicati	4
14	591	62 3		v	- 5 - 62 - 63 4 -	Γ.	4
15	591	62.3	117	9	US-07-634-	Sequence 4, Application	4
16	591	62.3	117	9	US-07-634-	72,	4.58e-39
17	591	62.3	117	9	US-07-634-	104,	4.58e-39
18	591	62.3	117	^	US-08-474-	4, Ap	4
19	591	62.3	117	7	US-08-487-	15,	4
20	591	62.3	117	7	US-08-487-	72,	4
21	591	62.3	117	٢	US-08-474-	Sequence 104, Applicat	4
22	591	62.3	117	۲-	US-08-474-	72.	4

23 591 62.3 117 7 TR-OR-487. Sequence 4, Applicatio 4.58e-39 24 597 61.9 12 12 PCT-USS9-0 Sequence 104, Applicatio 9.82-39 25 553 58.3 128 7 C.08-487. Sequence 110, Applicatio 9.82-39 26 553 58.3 128 7 US-OR-481. Sequence 12, Applicatio 1.31e-36 29 545 57.4 140 11 PCT-US99-1 Sequence 12, Applicatio 1.59e-34 29 546 57.4 140 11 PCT-US99-1 Sequence 12, Applicatio 1.59e-34 31 53.5 56.9 119 13 PCT-US99-1 Sequence 12, Applicatio 1.59e-34 32 531 56.0 116 6 US-OR-487. Sequence 6, Applicatio 1.59e-34 33 531 56.0 116 6 US-OR-474. Sequence 6, Applicatio 4.11e-34 35 531 56.0 116 6 US-OR-647. Sequence 6, Applicatio 4.11e-34 35 526 55.4 121 6 US-OR-487. Sequence 5, Applicatio 1.06e-33 36 526 55.4 121 6 US-OR-474. Sequence 53, Applicatio 1.06e-33 37 526 55.4 121 6 US-OR-487. Sequence 53, Applicatio 1.06e-33 38 526 55.4 121 7 US-OR-487. Sequence 53, Applicatio 1.06e-33 41 523 55.1 121 3 PCT-US95-0 Sequence 53, Applicatio 1.06e-33 42 525 55.4 121 6 US-OR-487. Sequence 53, Applicatio 1.06e-33 44 55.5 55.4 121 6 US-OR-487. Sequence 53, Applicatio 1.06e-33 45 51.5 50.0 116 6 US-OR-487. Sequence 53, Applicatio 1.06e-33 45 526 55.4 121 7 US-OR-487. Sequence 53, Applicatio 1.06e-33 47 528 55.4 121 12 3 PCT-US95-0 Sequence 13, Applicatio 1.06e-33 48 51.5 50.0 119 13 PCT-US95-0 Sequence 13, Application 1.06e-33 48 51.6 51.7 45 51.8 PCT-US95-0 Sequence 13, Application 3.99e-33 49 51.8 54.6 97 13 PCT-US95-1 Sequence 13, Application 2.6e-33 40 528 55.4 120 70 89 528 52 62 62 62 62 62 62 62 62 62 62 62 62 62	THEOUGH TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN A TITLE OF INVENTION: THEREOF NUMBER OF SEQUENCES: SUPERSONDENCE ADDRESS: ADDRESSEE: Seensley Horn Jubas & Lubitz STREET: 1880 Century Park East - Suite 500 GITY: Los Angelss STATE: California COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA COMPUTER: PROPY disk COMPUTER: PROPY disk COMPUTER: PROPY COMPUTER: PROFO COMPUTER
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US-08-844-215-7.rai

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COUNTRY:
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                                                                           SEQUENCE
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  APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIRODIES
                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG
                                                                                                                9
                                                                                                                                                                                 61 QKFQGRVTITADESTNTAYMELRSLRSDDTAMYYGAKEGYGDY-GR-P-FD-F--WGGGT 114
                                                                                                                                  1 VHLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVPQAPGGGIEWMGGIIPIFGGANYA 60
                                                                                                                                                   2 VQLLESGSEVKKPGSSVKVSCPASGSPPSYNFNWVPQAPGQGLEWMGTTPMFGTANYA 61
                                                                                                               7; Gaps
                                                                                             Length 120
                                                                                           Score 635; DB 11; Length 120
Pred. No. 1.04e-42;
15; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Pelease #1.0. Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MBER: PCT/US93/10555
29-0CT-1993
                                                                                                                                                                                                                                                                                                                                            Application PC/TUS9310555
                                                      NAME/KEY: Peptide
LOCATION: 1..120
GCE 120 AA: 13008 MW; 78865 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                         Sequence 12, Application PC/THS0310555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: HOWENLS, SEACY L.
REGISTRATION NUMBER: 4842
REFERENCE/DOCKET NUMBER: FD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (619) 455-5100
TECEFAX: (619) 455-5110
TECEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: THEREOF NUMBER OF SEQUENCES: 51 CORPESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 120 amino acids
amino acid
   MOLECULE TYPE: paptide IMMEDIATE SOURCE: CLONE: RAS PEATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                     Best Local Similarity 73.8%;
Matches 93; Conservative
                                                                                             :86 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Los Angeles
California
                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                 PCT-US93-10555-12
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                                                                                                                                                                                                                                                                                                                                            Sequence 12,
                                               FEATURE:
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                                                                           SEQUENCE
                                                                                              Query Match
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                                                                                                                                                                                                                                                            5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Humanized Antibodies Against Leukeryter
TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                            Score 609; PR 11; Length 120;
Pred. No. 1.48e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                          19; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYFE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DGS/MS-DGS SPTWARF: Patentin Poloase #1.5, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JMBER: PCT/US95/01219
25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15270-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 45, Application prymograp19,
                                                                                                                                                     110N: 1..120
120 AA; 12984 MW; 80846 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE THE ST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEG ID NO: 45:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER - US UP
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/LOCKET NUMBER -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Smith, William L.
REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                         peptide
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READARLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                 Query Match
Best Local Similarity 72.0%;
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       San Francisco
California
         MOLECULE TYPE: Deptimal MMEDIATE SOURCE: CLONE: BOR PEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                              NAME/KEY: Peptide
LOCATION: 1..120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT US95-01219-45
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60 YAQKFQGRVIITADESTATGYMELSSLRSEDTAVYYCAMPYPKHCSRGSC-WG--WFDPW 116
                                                                                                                                                                                                            61 YAQKFQGRVTITADISISTAYMELSSLPSEDTAVYYCAPA-PGYGSGGGGYPGDYXFDYW 119
                                                                                                                       15; Mismatches 16; Indels 5; Gaps
                                                                                                                                                     1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMGWINPYGNGDTN 60
                                                                                                                                                                               1 EVQLLESGSEVKKPGSSVKVSCRASGGSFRSYNFNWVRQAPGQGLEWMGGIIPM-FGTAN 59
                                                                                             Score 605, DB 13, Length 129,
Pred, No. 3 186-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE PATCHEL RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217.918
FILING DATE: 24-MAR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SMITH, Willialm M
PEGISTRATION NUMBER: 30, 223
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NOF $356-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LAKE, PHILIP
APPLICANT: LAKE, LARS
TITLE OF INVENTION: HUMAN ANTIBODIES ACAINST
TITLE OF INVENTION: HUMAN ANTIBODIES ACAINST
TITLE OF ENVENTION: VAPICELLA-ZOSTEP VIPUS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                     147 AA
                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAT AA; 15801 MW; 123306 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                   MOLEGULE TYPE Protein
FENCE 129 AA; 13930 MW; 96169 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08217918
Patent No. 5506132
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/NR21791R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 amino acids
129 amino acids
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                       STRANDEDNESS: single
TOPOLOGY linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                             Query Match 63 8%,
Best Local Similarity 72 3%;
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 379 Lytton
CITY: Palo Alto
STATE: California
COUNTRY: US
              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                 120 GQGTLVTVSS 129
                                                                                                                                                                                                                                                                                           117 GOGTLVTVSS 126
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LENGTH:
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                                                                  SEQUENCE
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Score 604; DB 6; Length 147; Pred. No. 3.85e-40;

63.6%;

Best Local Similarity

Query Match

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61 AQKRQSEVITIADESTATGYMELSSLESELTAVYYCAMPYPKHTSPSSLWGWF--DFWGQ 118
                                                                                  80 ACKFGGEVIISADASISTAYMELSSLPSDDTAMYYGAFDITAFGAAPTFLNFYGMDVWGQ 139
                                                 1 EVQLLESGSEVKKPGSSVKVS/PASGGSFRSYNFNWVPQAPOGGSLEWMGGIIFMFGTANY 60
                           20 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSNFAISWVRQAPGGGLEWMGRIMPLFVTSTY 79
2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGRIIPILGIANY 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O, Gaps
                                                                                                                                                                                                                                                                                                                                         Sequence 55, Application revised.
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TILLE OF INVENTION: Transgenic Non-Human Animals Capable of
TILLE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.7%; Score 595, DB 10; Length 102,
larity 82.5%; Pred No 2.146-39;
Conservative 12, Mismatches 5, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: William M. Smith
STREET: One Market Flata, Steuart Tower, Suite 2000
STREET: Can Prancisco
STATE: California
84; Conservative 21; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                 102 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT/US92/06185
                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                       Sequence 55, Application PC/TUS9206185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
SENCE 102 AA; 10940 MW; 55781 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEFERENCE/DOCKET NUMBER 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 87654
                                                                                                                                                                                                                                 STANDARD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-543-5043 INFOPMATION FOP SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
FILING DATE: 199108
CLASSIFICATION:
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Matches 80, Conserv
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PCT-US92-06185-55
                                                                                                                                             140 GTTVTVSS 147
                                                                                                                                                                        119 GTLVIVSS 126
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COUNTRY:
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                                                                                                                    Sequence 63,
                                                                  01-JAN-1900
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 595; DB 7; Length 102;
Pred. No. 2.140-39;
12; Mismatches 5; Indels 0; Gaps
                                                                                                                                                                                                APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M
TITLE OF INVENTION: Transqenic No. 5661016-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                            SSEE: Townsend and Townsend Khourie and Crew :: One Market Plaza, Steuart Tower, Sulte 200 San Francisco California
                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1 0, Version #1.25 CURRENT APPLICATION DATA
                                                  102 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCA 101
61 AQKFQGRVTITADESTATGYMELSSLRSEDTAVYYCA 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA -
APPLICATION NUMBER: US 07,990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA -
                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/053,131
FILING DATE: 26-APR-1993
CLASSIFICATION: 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 07/853,408
                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: TRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
SEQUENCE 102 AA; 10940 MW; 55781 CN;
                                                                                                                                                       Sequence 63, Application US/08053131 Patent No. 5661016 GENERAL INFORMATION:
                                                                                                                               Sequence 63, Application US/08053131
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TELECOMMUNIONTON INFORMATION-
TELEPHONE: 415-326-2400
TELEFAX- 415-35-2422
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-1991
                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS.
                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS - ADDRESSE: Townsend
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Best Local Similarity 82.58:
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM-
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                 US-08-053-131-63
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STATE: C
COUNTRY
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                                                                                                        01-JAN-1900
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5 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVPQAPGQGLEWMGP11F1LG1ANY 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 0; Caps
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Pred. No. 2.14e-39;
12; Mismatches 5; Indels (
                                                                                                                                                                                                                              APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
CORPRESPONDENCES: 152
                                                                                                                                                                                                                                                                                                                                                                        E: William M. Smith
One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Polease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC1/US92/10983
FILLIG DATE: 19921217
CLASSIFICATION:
TO2 AA
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PPT.
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                                                                                                                                                                                 63, Application PC/TUS9210983 INFORMATION:
                                                                                                                                       Seguence 63, Appliration Pr/THS9210983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-EGS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
JENCE 102 AA; 10940 MW; 55781 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 55, Application US/07834539A
Patent No. 5633425
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-326-2422
INFORMATION FOR SEG ID NO: 63:
SEQUENCE CHAPACTERISTICS:
STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTOPNEY/AGENT INPOPMATION:
NAME: Smith, William M.
PEGISTRATION NUMBER: 20.3
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AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 82.5%;
Matches 80; Conservative
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APPLICANT: Lonber
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PCT-US92-10983-63
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RESULT
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APPLICANT: Kay, Robert M.

TIȚLE OF INVENTION: Transgenic No. 5633425-Human Animals Capable of
TITLE OF INVENTION: Producing Heterologous Antibodies
CORRESPONDENCES: 77

CORRESPONDENCE ADDRESS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVQLIESGSEVKKPGSSVKVSGPASGGSFPSYNFNWVPGAPAGGTEWMGGTTPMFGTANY EF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CO, Man Sung
APPLICANT: SCHWEIDER, William P.
APPLICANT: LANDOLET, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMIN'GLORIINS
NUMBER OF SEQUENCES: 113
                                                          SSEE: William M. Smith

T. One Market Plaza, Steuart Tower, Suite 2000
San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 102;
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ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue
                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IRM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pelease #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 595; DB 7;
Pred No 2 14e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Mismatches
                                                                                                                                                                                                                               FILING DATE. 1992026
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REPERBUE/POOKET NUMBER: 14643-5
TELECHONE: 415-543-9600
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                     APPLICATION NUMBER: US/07/834,539A FILLING DATE: 19920205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPT;
                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
SEQUENCE 102 AA; 10940 MW; 55781 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/08474040 Patent No. 5593761 GENERAL INFORMATION: APPLICANT: QUEEN, Cary L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Application US/08474040
                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHAPACTEPISTICS
                                                                                                                                                                                                                                                                                                                                                                               102 amine acids
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                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 62.7%;
Local Similarity 82.5%.
Les 80; Conservative
                                                                                                                                         COMPUTER READABLE FORM.
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                         AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                 USA
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                                                                                                                            94105
                                                                ADDRESSEE:
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                                                                                                                 COUNTRY:
                                                                              STREET
                                                                                                                                                                                                                                                                                                                                                                               LENGIH
                                                                                                      STATE:
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                                                                                                                                                                  MEDIUM TYPE: FINEPRY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin PolosyMs-10,
SOFTWARS: Patentin PolosyMs-10,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/Ng/474,040
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DESC-1990
APPLICATION NUMBER: US 07/534,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Smith, William M
REDISTRATION NUMBER: 30.23
PEREPROFCORET NUMBEP: 11823-002500
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2422
INFORMATION FOR SEC 11 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 67/319,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBEP: US 07/290,975
FILING PATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
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Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: OCHNEIDER, William P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1.117
OTHER INFORMATION: /note= "Eu h
UTHER INFORMATION: sequence."
NCE 117 AA, 12472 MM, 77871 CN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 104, Application US/08477728.
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SCHNEIDER, William P.
SELICK, Harold E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 amino acids
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                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 79.0%;
Matches 79, Conservative
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California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                        94303
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                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH:
STATE:
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US-08-844-215-7.rai

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APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED
                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 62.3%;
Best Local Similarity 79.0%;
Matches 79; Conservative
                                                                                                 COMPUTER READABLE FORM:
                      NUMBER OF SEQUENCES:
                                                  STREET: Two Embarc
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: un
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                                                                                         94111
                                                                                                                                        SOFTWARE:
                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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     TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNGLOBLINS
                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTEF: INP PC compatible
COMPUTEF: IBM PC compatible
COMPUTEF: Datem: PC-Dos/Ms-Dos
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFFCATION: 424
                                  Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AQKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCAGGY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AQKFQGRVTITADESTATGYMELSSLRSEDTAVYYCAMPY 100
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                                            Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117
                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION NUMBER: US 07/590,274
PRILING DATE: 28-SEP-1990
PRICK APPLICATION NUMBER: US 07/310,252
PRICK APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRICK APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
FILING DATE: 28-DEC-1988
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                  E TYPE: peptide
117 AA; 12472 MW; 77871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08477728.
                                                                                                                                                                                                                                                                                                                NAME: Smith, William M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 104
                                                                                                                                                                                                                                                                                                                                                                                              117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
               NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                       Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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                                    ADDRESSEE:
                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                             STREET:
                                                                 STATE:
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1 EVOLLESGSEVKKPGSSVKVSCRASGSFRSYNFNWVRQAÞGOGLEWMGGIIPMFGTANY 60
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LOCATION: 1.117
LOCHER PREMATION: Anote= "Variable region of the human
OTHER INFORMATION: El antibody heavy chain."
NCE 117 AA: 12472 MW: 77871 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 591; DB 6; Length 117;
Pred: No. 4.58e-39;
IMPROVED HUMANIZED IMMUNOGLOBLINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                  Patentin Release #1.0, Version #1.25
                                             CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AQKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCAGGY 100
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                                                                                           Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 30,423
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                   CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310 or FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 326-2400
TELEFAX. (415) 326-2422
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                               113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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NO
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US-08-477-728-72
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                                                                     01-JAN-1900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EVOLLESGSEVKKPGSSVKVSCPASGSSPPSYNFNWVPQAPGGGLEWMSGIIPMFGTANY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Mismatches 10; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1.117
OTHER INFORMATION: /note= "Eu heavy chain amino acid
OTHER INFORMATION: sequence."
NCE 117 Asy, 12472 MW: 77871 CN;
                        Sequence 15, Application US/08477728
Patent No. 558508
GENERAL INFORMATION:
APPLICANT: GUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 117;
                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                       E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 62.3%; Score 591; DB 6; 1
Best Local Similarity 79 0%; Pred No 4 5%-39;
Matches 79; Conservative 11; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                      CLASSIFICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290.975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
ANDELSON NUMBER: US 07/290.975
FILING DATE: 13-FEB-1989
Sequence 15, Application US/08477728
                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                          STREET: Two ...
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
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                                                                                                                                                       ADDRESSEE:
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1 QVQLVQSGABVKKPGSSVKVSCKASGATESKSALIWVAQABGQGLBWAGGIVPMFGPPW 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                      Sequence 72, Application US/08477728
Patent No. 5585089
GENERAL INPORMATION
APPLICANT: OUSEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMINOGLOBLINS
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 62.3%; Score 591; DB 6; Length 117;
Best Local Similarity 79.0%; Pred. No. 4.58e-39;
Matches 79; Conservative 11; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC_compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Pelease #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AQKFQGRVTITADESTATGYMELSSLRSEDIAVYYCAMPY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AQKFQGPVTITADESTNTAYMELSSLRSEDTAFYFCAGGY 100
                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew STREET: Two Embarcadero Center, 8th Floor
117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Smith, William M
FEGISTRATION UNBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSPECATION: 44
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: US 07/710,252
FILING DATE: 13-FEB-1999
PRIOR APPLICATION NUMBER: US 07/710,252
FILING DATE: 13-FEB-1999
PRIOR APPLICATION NUMBER: US 07/710,252
FILING DATE: 28-DEC-1988
ATTERNEY AGENT INFORMATION:
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JENCE 117 AA: 12472 MW; 77971 CN;
                                                                                                                                                 Sequence 72, Application US/08477728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 326-2400
TELEPAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 72:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 117 amino acids
amino acid
STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
SOFTWARE: Patentin
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1 EVQLLESGSEVKKPGSSVKVSCPASGGSFPSYNFNWVPQAPGQGLFWMGGIIPMFGTANY 60
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APPLICANT:
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                                                                                                                                                                                                                                           01-JAN-1900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1..117
OTHER INFORMATION: /note= "Eu heavy chain amino acid
OTHER INFORMATION: sequence."
NCE 117 AA: 12472 MW: 77871 CN:
                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOSLUBELINS NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 591; DB 6; Length 117; Pred. No. 4.58e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O7/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION 1424
PRIOR APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SFP-1990
PFLOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/310,552
FILING DATE: US-DEC-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: US-DEC-1988
ATTONEVAGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue
                     117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 11823-002500
                     PRT;
                                                                                                                                                                                               Patent No. 5530101
CENERAL INFORMATION:
APPLICANT: CO. Man Sunq
APPLICANT: SCHNEIDER, William P.
APPLICANT: INTODER: Nicholas F.
APPLICANT: LANDOLE!, Nicholas F.
                                                                                                                                                                              Sequence 15, Application US/07634278
                                                                                                                                          Sequence 15, Application US/07634278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 326-2400
TELERAX: (415) 326-2422
INPORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                             SELICK, Harold E.
                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Smith, William M
REGISTRATION NUMBER: 30
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MEDIUM TYPE: Floppy
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California
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Matches 79; Conserv
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J 14
US-07-634-278-15
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                                                                                                 01-JAN-1900
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                                                             XXXXXX
RESULT
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3 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSRSAIIWVRQAPGTGLEWMGGIVPMFGPNY 60

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/note= "Variable region of the human
En antibedy beary chain."
                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                       : Townsend and Townsend Khourie and Crew 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DC5/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
61 AQKFQGRVTITADESTNTAYMELSSLRSEDTAFFCAGGY 100
                       61 AOKFOGRVTITADESTATGYMELSSLRSEDTAVYYCAMPY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11823-002500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 67/590,274
FILING DATE: 28.5EP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 67/310,252
FILING DATE: 13.FEB-1989
PRIOR APPLICATION ATA:
APPLICATION NUMBER: US 67/290,975
FILING DATE: 28-DEC-1988
                                                                          PRT;
                                                                                                                                                                                                                      CO, Man Sung
SCHNEIDER, William P.
LANDOLFI, Nicholas F.
COELINDE, Kathleen L.
SELICK, Harold E.
                                                                                                                                                                       Sequence 4, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary I..
                                                                                                                                                  Sequence 4, Application US/07634278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Smith, William M
REGISTRATION NUMBER: 30,223
PEFERENCE/POCKET NUMPER: 119
IELEPOMMUNICATION INCORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-242
INFORMATION FOR SEO 1D NO: 4:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 117 amino acids
amino acid
                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Protein LOCATION: 1..117 OTHER INFORMATION: CTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                     94301
                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
STREET: 37
                                                                         US-07-634-278-4
                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
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SQ SEQUENCE 117 AA; 12472 MW; 77871 CN;

Query Match 62.3%; Score 591; DB 6; Length 117; Best Local Similarity 79.0%; Pred. No. 4.58e-39; Matches 79; Conservative 11; Mismatches 10; Indels 0; Gaps

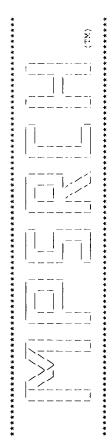
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Search completed: Tue Feb 24 07:42:57 1998 Job time: 14 secs.

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Release 2 1D John F Collins, Riocomputing Pescarch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07.15:35 1998, MasFar time 10.72 Seconds 163.248 Million cell updates/sec Run on:

Fabular output not generated

Description: Perfect Score:

... GSCWGWFDPWGQGTLVTVSS 126 >US-08-844-215-7 (1-126) from US08844215 pep 949 1 EVQLLESGSEVKKPGSSVKV. Sequence:

PAM 150 Gap 11 Scoring table:

111726 seqs, 13889129 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

lipart1 2:part2 3:part3 4:part4 5:part5 6:part4 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 3:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 a-geneseq30

Mean 30 601; Variance 151.366; scale 0.202 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length	DB	QI	Description	Pred. No.
-	773	81.5	481	Ŋ	R24442	Sequence of antibody	2.26e-54
CI	678	71.4	₩.	v.	F31023	Antibody D heary chai	5 526-46
m	635	6.99	120	σ.	P54796		1.07e-42
4	634	8.99	123	C1	W19887	011	1.30e-42
S	629		98	C1	R72068	eqion.	3.43e-42
9	621	65.4	(1) (1)	C.1	W19838	CEA specific antibody	1.620-41
7	620	65.5	C.	۲. در	W19885	CEA-specific antibody	1.976-41
6 0	619		6.51	CI	w1988a	CEA-specific antibody	2 400-41
σ	617	92	.23	۲,	W19881	ţ.	3.526-41
	604	63.6	147	12	R65019	93KA9 anti-Varicella	4.366-40
11	603	63.5	249	14	R77510	Humanised 5G1.1 VH +	5.30e-40
12	598	e.	119	53	W13536	Anti-melanoma antibod	1.390-39
13	595	62.7	96	1;	P72059	HV1263 VH region.	2.49e-29
14	595	62.7	117	۲	R38623	Human heavy chain V r	2.49e-39
15	595	62.7	117	₹	R22358	Frotein encoded by th	2.49e-39
16	595	62.7	117	20	W03950	DNA fragment vh49.8,	2.49e-39
17	592	62.4	249	14	R77615	Humanised 5G1.1 VH +	4.45e-39
18	591	62.3	117	C3	R24104	Human antibody Eu hea	5.40e-39
19	591	62.3	2.13	ur:	R28742	Heavy chain variable	5.400-39
20	587	61.9	122	14	P76964	HSV-neutralising anti	1.170-38

1.42e-38 1.72e-38 3.74e-38	.78e-3 .78e-3	62e-3	. 23e-3 . 65e-3	.90e-3 .90e-3 .72c-3 .73e-3	.02e-3	2.21e-34 2.67e-34 2.67e-34	444
Hy region of human rh Humanised CDR-grafted SpA-reactive IgM heav Monoclonal antibody S	nanised CDR-grafte nanised 5G1.1 VH + 1VV chain variable	manised C4G1 Ig h manised C4G1 Ig h	eavy chain variable re-5A8 humanised he	Humanised mouse DRG-2 PPEG-200 Humanized an Human anti-tumour ant OF7HL.2 VH-1 H Chain.	ed VLA-4 ed alpha- mal antib	Mutated human VNI gen CY1748RHB VH region. Heavy chain variable	Chimeric anti HIV ant Humanised heavy chain Heavy chain variable
R25325 R77616 R54795 845610	0 1 0	900	0.00	とい キア	200	27.2	8 4 6
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4444 4444							

ALIGNMENTS

RESULT	eri :
d K	R24442 standard; Protein; 481 AA. R24442
DI DI	02-JAN-1992 (first entry)
DE	Sequence of antibody molecule 1961.
X (Antibody; immunoglobulin G1.
so	sapiens.
E I	
FI	
-4 F	
⊣ £	/note= Substn to create grycan addition site? Nin difference :10
- L	MISC_UILLELENCE SIO
, <u>F</u>	
4 E	Another and the second of the
ΕH	
FI	/note= "see above"
БŢ	Misc_difference 329
FT	/label= N
FI	>
ΕĿ	Misc_difference 331
FI	/label= S
딘	/note= "see above"
ыŢ	Misc_difference 356
FI	/label= N
E 4	/pote= "see above"
E.	Misc_difference 369
FI	/label= N
E-	/note= "see above"
Ľ.	W09209204.
J.	11.JCN.1992.
다	
4	
ЬA	-14
Id	Seed B, Walz G;
D.P.	WPI; 92-216789/26.
S. H.	N-FSDB, Q25443.
ΡŢ	adhesion
PT	ing chronic inflammation, rheumatoid arthr
ΡŢ	psoriasis, etc.
PS	Disclosure; Fig 1; 46pp; English.
ပ္ပ	ars no
Ŋ	cule including
Ç	chains (see P24442

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61 AQKFQGRVTITADESTATGYMELSSLRSEDTAVYYCAMPYPKHCSPGSCW-GWFDPWGGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 aqkfqgrvtitadeststaymelsslrsedtavyycardngaycsqqscysgwfdpwgqg 144
additional N-linked glycosylation sites are introduced at locations which impair complement fixing and For ecceptor binding ability. They are preferably located in the CPD region of the TR molecule. Antibodies bearing multiple sially1-Lex determinants are useful for disrupting undesirable interactions between cells or proteins. Disrupting this interaction has therapeutic applications, for example, in minimising inflammation following tissue injury.
                                                                                                                                                                                                                                                                                                                                                                                                       25 gvglvgsgaevkkpgssvkvsckasggtfssyaiswvrqapggglewmggiipifgtany 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLLESGSEVKKPGSSVKVSCPASGGSFPSYNFNWVRQAPGGGLEWMGGIIPMFGTANY 60
                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heavy; light, chain; antibody, D, monoclonal, peripheral, blood, lymphocyte; hepatitis A virus; HAV; sero; positive; patient; murine; B5B3; polyadenylated; cDNA library; human; kappa; L; H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prodn. of recombinant primate antibodies - useful for treating infections caused by hepatitis A, B and C, herpes, cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,
                                                                                                                                                                                                                                                                              Score 773; DB 5; Length 481;
Pred No 2 26e-54;
                                                                                                                                                                                                                                                                                                                                          11; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R31023 standard; Protein; 476 AA.
                                                                                                                                                                                                                                                                              Query Match 81.5%;
Best Local Similarity 82.7%.
Matches 105; Conservative
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"Signal peptide"
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15-JUL-1991; GB-015284.
01-AUG-1991; GB-016594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody D heavy chain.
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/label- CDR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FR4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                        Sequence
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arthritis etc.
Disclosure: Fig 2: 35pp; English.
Disclosure: Fig 2: 35pp; English.
The sequences given in P31023 24 represent the beavy and light chains of Antibody D respectively. Antibody D is a monoclonal antibody which was derived from peripheral blood lymphocytes from a hepatitis A virus (HAV) sero positive patient. Antibody D is closely related in nature to murine antibody B5B3. Total RNA was isolated from antibody D expressing cells and polyadenylated RNA was extracted. These polyA RNA's were used to prepare a cDNA library which was screened for human kape light (D) chains and two positive clones were detected.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 sqnfqqrvtitadkststahmeltslrsedtavyycatdryrqanfdrarv qwfdpwqq 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AQKEQGEVIIIADESIATGYMELSSLRSEDIAVYYCAM-PYPK-HCSRGSCWGWFFFWGO 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stimulating prodn. of variable region gene family restricted antibodies. Through B cell super-antigen vaccination bischosure; Page 78: 130pp; English.

A B-cell superantigen (SAg) is a fragment of SpA D domain that specifically binds the Fab portion of variable region restricted antibodies. The SAg is used to enhance production of VH, especially variable from 19 Faction of VH, especially VH, restricted Ass Touring attempts to identify SAgs, as sequences (ES484-80) of H chains from 19 Feactive with mod-SpA, and as and DNA sequences (ES4842-55) of VH regions of SpA binders obtained from combinatorial libraries were determined. IgM protein KAS is derived from the germline configuration of a VH quee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 qkfqqrrtitadestntaymelrslrsddtamyycakegygdy-qr-p-fd-f--wqqqt 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 OKFORKLITADESTALGYMELSSLESEUTAVYYJAMP-YPKHUSERSKUMRUPPWYQGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                  20 qmqvvqsgaevkkpgssvtvsckasqqtfsnyaiswvrqapqqqlewmqqiiplidtpty 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l vhlugegaerkkpgssrkusskasggifsspalsworga, ygglewmggipilgganya 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VQLLESGSEVKKPGSSVKVSCPASGGSFESYNFNWVRQAPGGGLEWMGGJIPMFGTANYA 61
                                                                                                                                                                                                                                                                                                                                                               i Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-0cT-1994 (first entry)
SpA-reactive IqM heavy chain clone KAS.
SpA domain D: Iq binding region; IqM: B-cell superantiqen; SAq;
superantiqen; heavy chain variable region; VH3 restricted antibody;
VH; protein-A; KAS; B-lymphocyte; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                       Match 71.4%; Score 678; DB 6; Longth 476; Local Similarity 71.1%, Pred. No. 2.526-46; es 91; Conservative on Mr. 2.526-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 635; DB 9; Length 120; Pred. No. 1.07e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 11; Indels
                                                                                                                                                                                                                                        havy (H) chain chans were also isolated.
- 476 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R54796 standard, peptide, 120 AA.
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Matches 97, Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39-00T-1992; US-969936,
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAY-1994.
29-OCT-1993; U10555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 qtlvtvss 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 GTLVTVSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 lutuss 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Silverman GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09409818-A.
                                                                                                                                                                                                                                                                      Seguence
                                                                                                                                                                                                                                                                                                                Query Match
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       qq
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/note= "comple
WO9720932-A1.
                                                                                    Homo sapiens.
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                                                                                                                                                         /label= CDR2
                                                                                                                             /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= CDR3
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                                                                                                                                                                     W09508336-A
                                                                                                                                                                                     30-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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This polypeptide sequence comprises the heavy chain variable region (YH), HBAIL, obtained by mutagenesis of the VH CDR3 of human carcinoembryonic antigen (hCBA)-specific antibody CEAS (see W19881). A claimed specific binding member (A) comprises an hCEA constant for hCEA of less than 1 x 10 -8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 cextracellular domain of hCEA and/or to cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include parings of WH and CU. Sequences from CEA1-7 (see W19876-85), or their CDR sequences.

The constant of the containts (See W19886-95) obtained by mutagenesis or chain shiffling. (A) is used to detect cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 aqkfqgrltitadeststaymelsslrsedtavyyca-q-anscnrsyyy-ymdvrgqgt 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 qvqlvqsqaevkkpqssvkvsckasgqtfsnspinwlrqapgqglewmgsiipsfgtany 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVQLLESGSEVKKPGSSVKVSCPASGSSFPSYNFNWVPQAPGGSLEWMGSIIPMFGTANY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 12; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutagenesis or chain shuffling. (A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Specific binding members for human carcinoembryonic antigen - bind to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells, used for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 634; DB 23; Length 123;
Pred. No. 1.30e-42;
                                                                                                                                         tumour marker; lung cancer; breast cancer; colon cancer; adenocarcinoma; diagnosis.
                                                                                                           CEA-specific antibody CEÁS VH mutant HBAll sequence.
Carcinoembryonic antigen; CEA; human; antibody; scFv;
                                                                                                                                                                                                                                         /note= "complementarity determining region 1"
Region 50 66
                                                                                                                                                                                                                                                                                   /note= "complementarity determining region 2"
Region
                                                                                                                                                                                                                                                                                                                                 "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Osbourn JK;
                                                                                                                                                                                                                                                                                                                                                                                                                                  (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                                                                                                                 Location/Qualifiers
                                                     T 4
W19887 standard; Protein; 123 AA.
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R72068 standard; Frotein, 98 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 66.8%;
Best Local Similarity 73.0%;
                                                                                             07-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Allen DJ, McCafferty JG,
WPI; 97-319779/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      11-0CT-1996; GR-021295
07-DEC-1995; GR-025004
23-MAY-1996; GR-010824
                                                                                                                                                                      Chimeric Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                        09-DEC-1996; G03043
                                                                                                                                                                                    Chimeric synthetic.
            121 LVTVSS 126
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                                                                                                                                                                                                                           /label= CDR1
                                                                                                                                                                                                                                                                      /label- CDR2
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                                                                                 W19887
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1 qvqlvqsgaevkkpgssvkvsckasggtfssyaiswvrqapggglewmggiipifgtany 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue and clones encoding autoimmune-associated immunoglobulin fragments were obtained. 13/15 clones of H chain (1961) genes showed homology to the closest germline genes. DB10 (389328) and bull53 (289328). The DNA (289329) and corresp. amino acid (R72070) sequences of the VH region of a representative clone, Sequence. 98 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                     Graves' ophthalmopathy-associated monoclonal antibody - produced by molecular cloning of immunoglobulin genes by PCR Disclosure; Page 68; 94pp; English.

L- and H-chain DNA was amplifted by PCR from Graves' orbital
                                         Graves ophthalmopathy associated immunoglobulin protein; orbital antigen; monoclonal antibody; heavy chain; H chain; variable region, autoimmunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 65.3%; Score 529; DB 12; Length 98; Local Similarity 86.6%; Pred. No. 3.43e-42; nes 84; Conservative 11; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour marker; lung cancer; breast cancer; colon cancer; adenocarcinoma; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carcinoembryonic antigen; CEA; human; antibody; scFv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CEA-specific antibody CEA6 VH mutant HBB11 sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "complementarity determining region 3"
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07-DFC-1995; GB-025004.

23-MAY-1996; GB-010824.

(CAME.) CAMBRIDGE ANTIROPY TECHNOLOGY.
Allen DJ, McCafferty JG, Osbourn JR.
                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                      22-SEP-1994; U10756.
22-SEP-1993; US-124469.
(NICH-) NICHOLS INST DIAGNOSTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T
W19888 standard; Protein; 123 AA.
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26-SEP-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                       Rapoport B;
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                                                                                                                                                        31..35
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09-DEC-1996; G03043.
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                                                                                                                                                                                                                                                                                                                                                     Mclachlan SM, Rap
WPI; 95-139383/18.
                       DP10 VH region.
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This polypeptide sequence comprises the heavy chain variable region (VH), HBB1, obtained by mutagenesis of the VH CDR3 of human carcinoembryonic antigen (hCBA)-specific antibody CEA6 (see W1981). A claimed specific binding member (A) comprises an hCBA specific antibody antigen binding domain that has a dissociation constant for hCBA of less than 1 x 10 - 8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 cextracellular domain of hCBA and/or to cell-associated hCBA over hCBA over soluble hCBA. Preferred (A) include pairings of VH and VL sequences from CEA1-7 (see W19876-85), or their CDR sequences, as well as CEA6 VH and VL variants (see W19886-95) obtained by mutagenesis or chain shuffling. An example of a claimed pairing is HBB11 VH with CEA6 VL. (A) is used to detect cells expressing hCBA, in vivo or in vitro, especially tumour cells for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 aqkfqgrltitadeststaymelsslrsedtavyycar-h-nh-nyelyyymdvwgqgt 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AQKFQGRVIITADESTATGYMELSSLRSEDTAVYYCAMPYPKHCSRGSCWGWFDPWGQGT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLLESGSEVKKPGSSVKVSCRASGGSFRSYNFNWVRQAPGQGLEWMGGIPMFGTANY 60
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                       Specific binding members for human carcinoembryonic antigen - bind
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                                      to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 65.4%; Score 621; DB 23; Length 123; Best Local Similarity 73.0%; Pred. No. 1.62e-41; Matches 92; Conservative 16; Mismatches 15; Indels 3
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CEA-specific antibody CEA6 VH mutant TO6D10 sequence.
Carcinoembryonic antigen, CEA; human; antibody; scFv;
tumour marker; lung cancer; breast cancer; colon cancer;
adenocarcinoma; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                       adenocarcinoma of the colon, lung or breast.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                   Claim 4; Fig 2; 128pp; English.
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11-OCT-1996; GB-021295.
07-DEC-1995; GB-025004.
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Chimeric synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                        123 AA;
WPI: 97-319779/29
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61 agkfggrltitadeststaymelsslrsedtavyyca-gcshnyel-yyy-ymdvwqqqt 117
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            This polypeptide seguence comprises the heavy chain variable region (VH), ToSD10, obtained by mutagenesis of the VH CDR3 of human carcinoembryonic antigen (hEA)-specific antibody CEA6 (see HISB41). A claimed specific binding member (A) comprises an hEA specific antibody antigen binding domain that has a dissociation constant for hERA of less than 1 x 10 -8 M, is non-cross-reactive with human liver cells, and preferred in the A3-83 extracellular domain of hERA angiver real-lassociated hFRA over hERA over soluble hERA Preferred (A) include pairings of VH and VL sequences from CEA1-7 (see W19876-85), or their CDR sequences, as well as CEA6 VH and VL variants (see W19876-95) chrained by mutagenesis or chain shuffling. Examples of claimed pairings are TOSD10 VH with TOSD12 or CEA6 VL. (A) is used to detect cells.
                                                                                                                                                                                                                                                                 expressing hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast
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                                                                                                                                                                                                                                                                                                                                            Match 55.3%; Score 620; DB 23; Length 123; Local Similarity 72.2%; Pred. No. 1.97e-41; es 91; Conservative 16; Mismatches 16; Indels
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CEA-specific antibody CEA6 VH mutant HBB6 sequence.
Carcinoembryonic antigen; CEA; human; antibody; scFv;
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50..66
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89..112
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W19889 standard; Protein; 123 AA.
Claim 4; Fig 2; 128pp; English.
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07-DEC-1995; GB-025004.
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Chimeric synthetic.
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1 qvqlvqsgaevkkpgssvkvsckasggtfsnspinwlrqapgqglewmgsiipsfgtany 60
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This polypeptide sequence comprises the heavy chain variable region (WH) of human carcinoembryonic antigen (hCEA)-specific antibody CEA6. W (T72126-32) and VL (T72133-35) gene sequences were obtained for anti-hCEA antibodies CEA1-CEA7 (see W19876-85). A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 ° 8 M, is non-cross-reactive with human diver cells, and preferentially binds to the A3-B3 extracellular domain of hCEA and/or to cell-associated hCEA over hCEA cver
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specific antibody antigen binding domain that has a dissociation constant for LGEA of less than 1 x 10 -8 m, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 extracellular domain of hCEA and/or to cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include pairings of VH and VL sequences from CEA-7 (see W19876-85), or their CDR sequences as well as CEA6 VH and VL variants (see W19886-95) obtained by mandagenesis or chain shuffling. An example of a claimed pairing is HBB6 VH with CEA6 VL (A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for diagnosing
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                                                                                                                                                                                                                                                           Query Match 65.1%: Score 618; DB 23; Leugth 123; Best Local Similarity 73 0%: Prod. No. 2 900-41; Matches 92; Conservative 15; Mismatches 16, Indels
                                                                                                                                                                                                   cancer, e.g. adenocarcinoma of the colon, lung or breast.
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Carcinoembryonic antigen; CEA, human, antibody, scFv;
tumour marker; lung cancer; breast cancer; colon cancer;
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23-MAY-1996; GB-010824
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09-DEC-1996; G03043
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D
                                                                                                                                                                                                                          Sequence
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claim 8; Fig 4B; 39pp; English.
A human anti-Varicella zoster virus monoclonal antibody was prepd.
Using the trioma method of Carberg et al. (1983) Hybridoma 2:361-367.
One resultant trioma neutralised VzV in the absence of complement.
This cell line, designated cell line TC93KA9, produced an antibody designated 93KA9 of the light and heavy chain variable region genes of the 93KA9 antibody were cloned using PCR. At least two heavy chain (gamma-1) and two light chain (kappa) specific clones were sequenced (see Q82749 & Q82750 respectively).
                                                                                                                                                                                                                                                                                    61 aqkfqgrltitadeststaymelsslrsedtavyycagr-shnyel-yyy-ymdvwgqgt 117
                                                                                                                                                                                                                 Score 617; DB 23; Length 123;
Pred. No. 3.52e-41;
16; Mismatches 16, Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Gaps
            sequences from CEA1-7, or their CDR sequences, as well as CEA6 VH and VL variants, including combinations of CEA6 VH with VL regions from CEA6, TCAGA4, TCAGA2, TCAGA2, LCAGA2, CAGA3 is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Varicella zoster virus; VZW; anti-VZW monoclonal antibody; 93KA9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-OCT-1995 (first entry)
93RA9 anti-Varicella zoster virus antibody heavy chain variable.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - used in a therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *Match* 63.6%, Score 604, DB 12; Length 147, Local Similarity 65.6%; Pred. No. 4.36e-40; es 84; Conservative 21; Mismatches 21; Indels 3
soluble hCEA. Preferred (A) include pairings of VH and VL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region 50..54
Tabel complementarity determining region (CDR) 69..85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key Location/Qualifiers
Protein 20.147
/label= mature light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sub:unit of varicella zoster virus prophylaxis of infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                      R65019 standard; Protein; 147 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glycoprotein II subunit; vaccine,
                                                                                                                                       Ouery Match
Best Local Similarity 72.2%;
                                                                                                                                                  65.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-1993; US-098479.
24-MAR-1994; US-217918.
(SANO ) SANDOZ PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           008241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ostberg L;
                                                                                                                123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 95-090612/12.
N-PSDB; 082750.
                                                                                                                                                                                                                                                                                                                                                   118 mvtvss 123
                                                                                                                                                                                                                                                                                                                                                                                    121 LVTVSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JUL-1994,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-0CT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'label= CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9504080-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R65019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lake P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          region.
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20 gvqlvqsgaevkkpgssvkvsckasggtfsnfaiswvrqapgqglewmgrimplfvtsty 79

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 Treating glomerulonephritis with antibody against complement C5 component - to inhibit complement induced cell lysis Example 11: page 119-122; 181pp: English.

A humanised CDR-grafted and framework sequence-altered Fd, 5G1.1 VH + IGHRL (R77610), includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. It can be co-expressed with a humanised light chain (R77612) in human 293 EDNA cells using encoding DNAs subcloned into vector APEX.3P (T08476). Such humanised recombinant antibodies retain the ability of MAb 5G1.1 to block human complement C5s generation and thus to reduce glomerular inflammation and kidney dysfunction associated with glomerulonephritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 aqkfqgrvtmtadtststaymelsslrsedtavyycar-yf-fgsspn-w-yfdvwgqgt 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AQKFQGRVIITADESTATGYMELSSLRSEDTAVYYCAMPYPKHCSRGSCWGWFDPWGQGT 120
                                                  61 AQKFQGRVTITADESTATGYMELSSLRSEDTAVYYCAMPYPKHCSRGSCWGWF--DPWGQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EVQLLESGSEVKKPGSSVKVSCRASGGSFRSYNFNWVRQAPGGGLEMMGGIIPMFGTANY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 qvqlvqsgaevkkpgasvkvsckasgyifsnywiqwvrqapgqglewmgeilpgsgstey 79
1 EVQLLESGSEVKKPGSSVKVSCRASGSSFRSYNFNWVRQAPGQGLEWMGGIIPMFGTANY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Gaps
                           80 aqkfqgrvtısadaststaymelsslrsddtamyycarditapgaaptplnfygmdvwgq
                                                                                                                                                                                                      numerical (Complement C5; hemolysis; kidney; glomerulonephritis; monoclonal antibody; antiinflammatory; antibody engineering; humanised antibody; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 603; DB 14; Length 249;
Pred No 5 30e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 17, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thomas IC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Matis L, Mueller EE, Nye SH, P, Springhorn J P, Squinto SP, Wilkins JA;
                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
ID W13536 standard; protein; 119 AA.
                                                                                                                                              T 11
R77610 standard; Protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.5%,
70 6%;
                                                                                                                                                                                 15-MAR-1996 (first entry)
Humanised 5G1.1 VH + IGHRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                          118..130
                                                                                                                                                                                                                                                                                                 . 249
                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1995; U05688.
02-MAY-1994; US-236208.
                                                                                                                                                                                                                                                                                                                         45..54
                                                                                                                                                                                                                                                                                                                                                   69..79
                                                                                                                                                                                                                                                                          . 19
                                                                                                                                                                                                                                                                                     /label- sig_peptide
                                                                                                                                                                                                                                                                                                             /label- mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang Y, Wilhim...
                                                                                                       119 GTLVTVSS 126
                                                                             140 gttvtvss 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 lvtvss 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 LVTVSS 126
                                                                                                                                                                                                                                                                                                                                       /label- CDR-H1
                                                                                                                                                                                                                                                                                                                                                              /label= CDR-H2
                                                                                                                                                                                                                                                                                                                                                                                      /label= CDR-H3
                                                                                                                                                                                                                                                                                                                                                                                                   WO9529697-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                09-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rother RP,
                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Evans MJ,
                                                                                                                                                                     R77610;
                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                            Region
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From 19: Page 75:76: 82pp; English.

Claim 19: Page 75:76: 82pp; English.

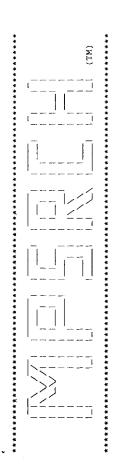
A process for isolating and synthesising human monoclonal anti-tumour antibodies has been produced. The process involves: (a) constructing at antibodies has been produced. The process involves: (a) constructing at cancer patient; (b) screening for anti-tumour antibodies in the page 10 page 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiqens for studying tumourigenesis or for use as anti-cancer vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The human antibodies have low immunogenicity in humans compared to murine monoclonal antibodies (MARS). Since the antibodies are isolated from fusion phage libraries, their affinity and specificity for a tumour cell line can be improved by genetic manipulations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 rvtitadkststaymelsslrsedtavyyca---r--g-ggrydafdiwgggtlvtvss 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 gglevkkpgssvkvsckasggtfssyaiswvrqapggglewmgqiipifqtanyaqkfqq 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Gaps
28-OCT-1997 (first entry) Ant: melanoma antibody 2-71 from VH antibody fusion phage library. Human; monoclonal antitumour antibody; peripheral blood lymphocyte; cancer; tumourigenesis; anticancer vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prodn. of human monoclonal anti-tumour antibodies - by screening a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 usion phage library produced using peripheral blood lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigen; monoclonal antibody; heavy chain; H chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Graves ophthalmopathy associated immunoglobulin protein;
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Pred. No. 1.39e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Mismatches
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(NICH-) NICHOLS INST DIAGNOSTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T 13
R72069 standard; Protein; 98 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           variable region; autoimmunity.
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Local Similarity 77.5%;
les 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               US-497647.
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22-SEP-1993; US-1244
                                                                                                                                                                                                                                                                                                                                                                                           28-JUN-1996; IB1032
                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-1995; US-497
(UYYA ) UNIV YALE.
Cai X, Garen A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HV1263 VH region.
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                                                                                                                                                                                                                                                                                         WO9702479-A2.
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                                                                                                                                                                                                                                Homo sapiens
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82.5%; Pred. No. 2.49e-39;
Artive 12; Mismatches 5; Indels 0; Gaps
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                                                                                                                                                                                                                                                                   5; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A human placental genomic DNA library cloned into the phage vector tambda FIX I was screened with the human VH1 family specific oligonucleotide Q44Me. Phage clone lambda 49 8 was isolated and a 6.1kb xbal fragment containing the variable segment VH49.8 was buckloned into pNU3 to generate plasmid pu49.8 A n 800bp region of this insert was sequenced (Q44185) and VH49.8 found to have an open reading frame and intact splicing and recombination sequence Q44185 was deduced from the coding sequence; the last 3 codons before the termination codon have not been translated.
                                                                                              tissue and clones encoding autoimmune-associated immunoglobulin fragments were obtained. 13/15 clones of H chain (1gG1) genes showed homology to the closest germline genes, pPt0 (2R9327) and hv1263 (089328). The DNA (289329) and corresp. amino acid (R72070) sequences of the VW region of a representative clone, OF7H1.2, are provided.
               N\text{-}PSDB_{\neq}\cdot Q69328. Graves' ophthalmopathy-associated monoclonal antibody - produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transgent non-human animals contq. immunoglobulin heavy chain trans gene - used to produce useful antibodies by isotype
                                               by molecular cloning of immunoglobulin genes by PCR
Disclosure; Page 69; 94pp; English.
L- and H-chain DNA was amplified by PCR from Graves' orbital
                                                                                                                                                                                                                                   Score 595; DB 12; Length 98;
Pred No. 2 496:39;
12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-NOV-1993 (first entry)
Human heavy chain V region VH49.8.
Immunoglobulin; IgG; heavy chain; minilocus transgene;
Isocype switching; H chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R38623 standard; Protein; 117 AA
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 82 5%
Matches 80; Conservative
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17-DEC-1991; US-810279.
18-MAR-1992; US-853408.
23-UUN-1992; US-904068.
(GENP-) GENPHARM INT INC.
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Matches 80; Conservative
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WFI; 95-139383/18.
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20 qvqlvqsgaevkkpgssvkvsckasggtfssyaiswvrqapgqglewmgriipilgiany 79
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The human placental genemic DNA library cloned into the phage vector lambda FIX II was screened with the human VHI family specific Oligonucleotide (See 022418). Phage clone lambda 49.8 was isolated and a 6.1 kb Xbai fragment contg. the variable segment VH49.8 subcloned into pNNN3 to generate plasmid pVH49.8. An 800 bp region of this insert was sequenced. VH49.8 was found to have an open reading frame which encoded the sequence shown.
                                                                                                17-AUG-1992 (first entry)
Protein encoded by the human heavy chain V region gene VH49.
Heavy chain; variable region; VH1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 62.7%; Score 595; DB 4; Length 117; Local Similarity 82.5%; Prod No. 2.496-39; hes 80; Conservative 12; Mismatches 5; Indels
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JI 15
R22358 standard; Protein; 117 AA.
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                                                                                                                                                                                                                                                                    19-MAR-1992.
28-AUG-1991; U06185.
29-AUG-1990; US-574748.
31-AUG-1990; US-575962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  I, Kay R,
13962/14.
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                                                                                                                                                                                                              Homo sapiens.
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Lonberg N,
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Release 2 1D John F. Collins, Biocomputing Pesearch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Run on:

Tue Feb 24 07-12-56 1998; MasPar time 8 23 Seconds 466.347 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score:

>US-08-844-215-6 (1-126) from (S08944215 pop 925 1 EVQLLESGPGLVKPSGTLSL......RMMLDAFDIWGQGTLVIVSS 126 Sednence:

PAM 150 Gap 11 Scoring table:

95051 seqs, 30469580 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Tranni 2 acn2 3 ann3 4 acn4 5 unanci 6 unanci 2 trundon 3 8 unann4 9 unann5 10 unann6 11 unann7 12 unann8 13 unann9 14 unann10 15 unann11 16 unann12 17 unenc

Mean 41.798; Variance 118.726; scale 0.352 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ouery Match Length	BB	QI	Description	Pred. No.
1	614	9	129	7	S44114	Iq heavy chain V req	3.47e-68
2	611	99	130	7	S31690	heavy chain V	
m	608		134	7	S54906	31 heavy chain	2.51e-67
4	598		86	7	S26905	e	•
'n	598	64.	98	7	S12419	heavy chain V	.75e-
9	597		139	7	\$31586	heavy chain V	yy-068 6
7	588	63.	123	^	830529	heavy chain V	1.81e-64
œ	585	63.	140	^	137782	-	4.86e-64
6	583		98	7	S12417	g	9.39e-64
10	583	63	ď	7	S25904	heavy chain V	9.39.1-64
11	581	62.	130	7	S30534	heavy chain V	1.81e-63
12	581		147	7	513519	heavy chain V	1.810-63
13	575	62	155	۲-	831512	heary chain -	1.30e·62
14	574		155	7	831511		1.80e-62
15	569	61.	146	7	809710		9.31e-62
16	267	61.3	86	7	S12413	Iq heavy chain V req	1.79e-61
17	567	61.	98	7	S26903	heavy chain v	1.79e-61
18	564		86	7	S12414	heavy chain V	4.80e-61
19	563	.09	135	7	S31604	heavy chain V	6 660-61
20	561	. 09	105	1	S44125	g lambda chain V	1 286-60

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CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 134 #checksum 1180
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                                                                                                        Tonnelle, C. submitted to the EMBL Data Library, June 1992 Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in feral liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3, Gaps
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                                                                                   Cuisinier, A.M : Gauthier, L ; Boubli, L.; Fougereau, M
22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Esposito, G.; Traboni, C. submitted to the EMBL Data Library, November 1994 Cloning and sequencing of cDNA coding for the variable domains of a human antibody against Hepatitis C virus
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#formal_name Homo sapiens #common_name man
08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                   #domain immunoglobulin homology #label IMM
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66.1%; Score 611; DB 7; Length 130;
Best Local Similarity 73.2%; Pred. No. 9.32e-68;
Matches 93; Conservative 12; Mismatches 19, Indels
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Matches 90; Conservative
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J. Mol. Biol. (1992) 227:776-798
The repertoire of human germline V(H) sequences reveals about fifty groups of V(H) seaments with different hypervariable
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FICATION #superfamily immunoglobulin V region: immunoqlobulin homolony
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FICATION #superfamily immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                    I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.;
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                                  Ig heavy chain V region (DP-70) - human (fragment)
#formal_name Homo sapiens #common_name man
22-Nov-1993 #sequence_revision 10-Nov 1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #title The smaller human V(H) gene families display remarkably
little polymorphism.
#cross-references MUID:90059975
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Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.;
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Ig heavy chain V region - human
*formal_name Homo saplens *common_name man
06-Jan-1995 *sequence_revision 06-Jan-1995 #text_change
16-Aug-1996
                                                                                                          S31586 #type fragment
Ig heavy chain V region - human (fragment)
#formal_name Homo sapiens #common_name man
22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
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submitted to the EMBL Data Library, October 1992
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                  51 npslksrvtisvdksknqfslklssvtaadtavyycar
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Best Local Similarity 71.0%;
Matches 88; Conservative
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*superfamily immunoglobulin V region; immunoglobulin homology
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#title Somatic diversification in the heavy chain variable region genes expressed by human autoantibodies bearing a lupus-associated nephritogenic anti-DNA idiotype.
#accession 137782
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EMBO J. (1989) 8:3741-3748
                                                                                                                                                                                                                                                                                                                          Ig variable region (VDJ) (clone T23-9) - human (fragment) #formal_name Homo sapiens #common_name man 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change
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Ig heavy chain V region (4.17) - human
#formal_name Homo sapiens #common_name man
18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
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heterotetramer; immunoglobulin
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#cross-references MUID:90059975
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CLASSIFICATION #superiamily immunoo
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FTCATION #superfamily immunoglobulin V region; immunoglobulin homology
IDS heterotetramer; immunoglobulin
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FICATION *superfamily immunoglobulin V region; immunoglobulin homology
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                                                                                                          1 qvqlqesqpglvkpsetls1tcvvsqgsisssnwwswvrqppgkglewigeiyhsgspny 60
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                                                                                                                                              1 EVQLLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSTIY 60
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#formal_name Homo sapiens #common_name man
22-Nov-1993 #sequence_revision 10.No:-1395 #text_change
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#formal_name Homo sapiens #common_name man
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
#length 98 #molecular-weight 10634 #checksum 6422
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                                  63.0%; Score 583; DB 7; Length 98; 81.6%; Pred. No. 9.39e.64.
rative 8; Mismatches 10; Indels
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lain V region - human
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Best Local Similarity 81.6%,
Matches 80; Conservative
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##cross-references EMBL:X56158
FICATION #superfamily immunoglobulin V region; immunoglobulin homology
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#formal_name Homo sapiens #common_name man
13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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          Score 581; DB 7; Length 130; Pred. No. 1 81e-63;
                                                              24; 183018
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Best Local Similarity 70.8%;
Matches 92, conservation
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                                                                                  *superfamily immunoglobulin V region; immunoglobulin homology
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Ig heavy chain V region - human
#formal_name HnV sapiens #common_name man
21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
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Pred. No. 1.80e-62;
20; Mismatches 19; Indels
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22; Mismatches 18; Indels
                                                                                                                                                                                                              Query Match 62.2%; Score 575; DB 7; Best Local Similarity 65.9%; Pred. No. 1.30e-62 Matches 83; Conservative 22; Mismatches 1
                                                                                                         heterotetramer; immunoglobulin
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*superfamily immunoglobulin V region; immunoglobulin homology
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Hapfnes-Jones, N.C.: Bye, J.M.: Beale, D.; Coadwell, J.
Biochem. J. (1990) 268:135-140
Nucleotide sequences and three-dimensional modelling of the
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18; Mismatches 26; Indels 1; Gaps
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Best Local Similarity 64.6%;
Matches 82; Conservative
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##residues 1.146
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, H K Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07:13:22 1998; MasPar time 5.58 Seconds 478.962 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-844-215-6 (1-126) from US08844215.pep 925 Description: Perfect Score:

1 EVQLLESGPGLVKPSGTLSL......RMMLDAFDIWGQGTLVIVSS 126 Sedneuce:

PAM 150 Gap 11 Scoring table:

59021 segs, 21219398 residues Searched.

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Mean 42 377; Variance 75 063; scale 0 565 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMAPIES

* 22 # :-	ry ch Length Di		Description	ion	
4 6				ż	6-200
5.4 14	S	HV2I_HUMAN	IC HEAVY	CHAIN PRECUR	2.40e-87
.9 11	S	HV2G_HUMAN	IG HEAVY	CHAIN V-II P	4 036-78
.6 11	Ŋ	HV60_MOUSE	IG HEAVY	CHAIN PRECUR	3.396-71
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.1 13	S	HV46_MOUSE	IG HEAVY	CHAIN PRECUR	4.340-66
.1 11	S	HV62_MOUSE	IG HEAVY	CHAIN PRECUR	4.256-64
14	S	HV43_MOUSE	IG HEAVY	CHAIN PPECUP	7 07p-64
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11	'n	HV40_MOUSE	IG HEAVY	CHAIN V REGI	3.13e-61
.7 11	ഗ	HV41_MOUSE	IG HEAVY	CHAIN V REGI	2.97e-59
.5 11	ĸ.	HVOS_CARAU	IG HEAVY	CHAIN PPECUP	8 17e-59
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0.3 11	'n	HV3F_HUMAN	IG HEAVY	CHAIN V-III	2.10e-56
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9.7 11	L	HV44_MOTTSE	IG HEAVY	CHAIN PPECHP	4 280-55
39.5	L	HV3C HIMAN	TO HEAVY	TTTT NINHU	170-51

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P06313.
01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAS! SPAUSNCE UPDATE)
01-NOV-1990 (REL. 16, LAS! ANNOTATION UPDATE)
1G HEAVY CHAIN PRECURSOR V-11 PEGION (APH-77)

RESULT

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ALIGNMENTS

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HVP_HUMAN STANDAPD; PPT; 129 AA. 901824. 21.JUL-1986 (PEL 01, CPEATED) 21.JUL-1986 (PEL 01, LAST SEQUENCE UPDATE) 21.JUL-1986 (PEL 01, LAST SEQUENCE UPDATE) 1G HEAVY CHAIN V-II REGION (WAH). HOWO SAPIENS (HUMAN). HOWO SAPIENS (HUMAN). 1G HEAVY CHAIN V-II REGION (WAH). HOWO SAPIENS (HUMAN). 1G HEAVY CHAIN V-II REGION (WAH). 1G HEAVY CHAIN V-II REGION (WAH). 1G HEAVY CHAIN WETAZOA: 1G HORATA: DEBUIPE B , LIN L -C , PUTNAM F.W.; PROC. WALL. ACAD. SCI. U.S.A. 79:2259-2284(1292). 1THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA PROTEIN. 1THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA PROTEIN. HSSR: PO1607: 1FGV. HSSR: PO1607: 1FGV. HSSR: A02099: D24UWA . 129 129 SEQUENCE 129 AA: 14117 WW. 25BAB2F5 CRC32;	Score 549: DB 5: Length 129; Pred No. 1 00e-95; 20; Mismatches 25; Indels 3: Gaps ReggpirrigyWgwirqppgkglowiggwyrgsiyy 51
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HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                           Score 512; DB 5; Length 146; Fred. No. 2.40e-87,
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MEDLINE: 78066916.
3 ANGL 1. AMZEL 1. POLJAK P.J.;
J. BIOL. CHEM. 253:586-597(1978).
1- THIS CHAIN WAS ISOLATED FROM AN IGGI MYELOMA PROTEIN.
PIR; A02100; GIHUNM.
PDB; 7FAB; 31-3AN-94.
IMMUNGLOBULIN V REGION: 3D-STRUCTUPE.
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BIOCHEMISTRY 16:3412-3420(1977).
                                                KUDO A., ISHIHARA T., NISHIMURA Y., WATANABE T.;
GENE 33:1891.189(1985).
PIR; A02101; GHUH2.
HSSP: P01825; 1FOV.
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01-JUN-1994 (REL. 29, LAST ANNOTAT:
IG HEAVY CHAIN V-II REGION (NEWM).
                                                                                    IMMUNOGLOBULIN V REGION; SIGNAL.
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Best Local Similarity 60.6%;
Matches 77; Conservative
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EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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COMPLEMENTARITY-DETERMINING 2.
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LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1990 (PEL. 15, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE HEDATE)
01-NOV-1990 (PEL. 16, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                   116 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDAT)
01-NOV-1990 (REL. 16, LAST NONOTATION UPDAT)
IG HEAVY CHAIN PRECUPSOR V PEGION (M315).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAMEWORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAMEWORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BALB/CJ;
MEDLINE; 89279149.
LEVY N.S., MALIPIERO U V., LEHROG, J. EXP. MED. 159.2007-2019(1989).
PIR; JT0509; HYMS31.
HSSP; P01825; 1BAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                   Similarity 66.3%; 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 59.2%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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48
48
53
67
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116
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64
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77
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87
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104
111
117 AA;
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85
40
116
116 AA;
                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    T 4
HV60_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 5
HV61_MOUSE
P18532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
DISULFID
NON_TER
SEQUENCE
                                                                                                                           SEQUENCE
                                                                                                                                                     Query Match
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                TURN
                                           TURN
                                                                                                                                                                                 Matches
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60 YNPSLNEPVEMSVLKSKE VVSLPLSSVIAAUTAVYVARSPIKMN PAPML-DAFDINGQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE: 77244979.
MEDLINE: 77244979.
MEDLINE: 77244979.
MARGALES M. N., SIVOL D., ZAKUT P.;
UNPOBLISHED RESULTS, CITED BY:
PADLAN E.A., DAVIES D.P., PECHT I., GIVOL D., WRIGHT C;
COLD SPRING HARB SWMP GOTANT. BROL 41.627-637(1977).
-1- THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT HAS
ANTI-DINITROPHENYL ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IC HEAVY CHAIN V PEGION (MOPC 315).
                                                                                                                                                                                          EUKAPYOTA, METAZOA, CHORDATA, VERTERRATA, TETRAPODA, MAMMALIA,
EUTHERIA, RODENTIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPLEMENTARITY-DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPLEMENTARITY - DETERMINING 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEMENTAPITY-DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
G -> GG (IN G295908).
G -> H (IN REF. 2).
GY -> YG (IN REF. 4).
N -> C (IN REF. 4).
MISSING (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDEINE: 74170779.
FRANCIS S H , LESLIE P G Q , HOOD L , BISEN H.N.;
PROC NATL. ACAD. SCI. U.S A 71:1123-1127(1974).
                                                                                                                                                                                                                                                                                                                         U.S.A. 74:5692-5696(1977).
                                                                                                                                                                                                                                                PINFPER A, HOPNE C., DOPPINGTON K 7, KLEIN M.; MOL. IMMUNOL. 26:431-434(1989).
                                                                                                                                                                                                                                                                                                                                                                       , ZEMELI P., BUPSTEIN Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15399 MW; 155A5E8D CRC32;
                                                                                                                                                        LAST ANNOTATION UPDATE)
                                                                                                                                                                  IG HEAVY CHAIN PRECURSOR V PEGION (MOPC 315).
MUS MUSCULUS (MOUSE)
                                                                                                       137 AA
                                                                                                                               CREATED)
LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAMEWORK 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAMEWORK 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FPAMEWORK 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAMEWORK
                                                                                                         PPT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P01789; 2FGW.
IMMUNOGLOBULIN V PEGION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                        79148758.
1 WOLF O ZEMELL !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M27638; G602707; -. EMBL; X07880; G295908; -. PIR; PL0102; AVMS35. HSSP; P01789; 2FGW.
                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                MEDLINE, 78094475.
JILKA R.L., PESTKA S.;
PROC. NATL. ACAD. SCI.
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548
1116
1116
1137
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1158
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01-AUG-1992 (REL. 23,
01-FEB-1996 (REL. 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102
123
137
137 AA;
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                                                                                                                                                                                                                                       MEDLINE; 8923835.
                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-31
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SCHECHTER I
                                    140 gt 141
                                                           119 GT 120
                                                                                                        HV46_MOUSE
P01822;
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                                                                                                                                                                                                                                                                                                                                               19 dvqlqesgpdlvkpsqslsltctvtgysitsgyswhwirqfpgnklewmgyihysgntsy 78
                                                                                                                                                                                                                                                                                                                                                                      1 EVQLLESGPGLVKPSGTLSLTCTVSGGSIP$SHWWSWVPQPPARALEWIGEVFFSGSTIY 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 419; DB 5; Length 147;
Pred. No. 1.57e-66;
26, Mismatches 34, Indels 2, Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 qvnlresgpalvkathtltltctfsglsvntrgmsvswirgppgkalewlaridwdddky 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVQLLESGPGLVKPSGTLSLTGTVSGGSTPSSHWW-SWVPGPPGGKGLEWIGEVEFSGSIL 59
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG HEAVY CHAIN V-II REGION (SESS) V SEGMENT.
          MUS MUSCULUS (MOUSE).
EUKAPYOTA: META70A: CHOPDATA: VEPTERPATA: TETPAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMO SAPIENS (HUMAN).
EUKAPYOTA: METAZOA: CHOPDATA: VEPTEBPATA: TETPAPODA: MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                             IG HEAVY CHAIN V PEGION (1843)
                                                                                                                                                                                                    COMPLEMENTARITY-DETERMINING 1. FRAMEWORK 2
                                                                                                                                                                                                                          COMPLEMENTARITY-DETERMINING 2
                                                                                                                                                                                                                                                                                                Score 431; DB 5; Length 116; Pred. No. 3.41e-69;
                                                                                                                                                                                                                                                                                                                         18; Mismatches 21; Indels
                                                                                         LEVY N.S., MALTPIERO U.V., LERECQUE S.G., GEARHART P.J., EXP. MED. 169:2007-2219(1989)
-1- THIS SECONDER BELONGS TO THE VH3660 SUBFAMILY.
PIR: JTOSOB HWESIB.
HSSP: P01825; IBAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 84298107.
TAKHASHI N, NOWA T, HONJO T;
PROC. NATL ACAD SCI. U S A RI-5194-5198(1984)
PIR, A02090; GZHUCS.
HSSP; P01772; 1GGB.
                                                                                                                                                                                                                                                                                                                                                                                             79 npslksrisitrdtsknqfflqlnsvttedtatyycar 116
                                                                                                                                                                                                                                                                                                                                                                                                                   61 NPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCAR 98
                                                                                                                                                                                                                                                                         13158 MW; 10E4EE67 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-AUG-1987 (PEL. 05, CREATED)
13-AUG-1987 (PEL. 05, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
1G HEAVY CHAIN PPECURSOR V-II REGION (SESS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16323 MW; 0994FFF4 CPC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 AA
                                                                                                                                                                                                                                                  BY SIMILAPITY
                                                                                                                                                                                                                                        FPAMEWORK 3
 IG HEAVY CHAIN PRECTIFICION (1843)
                                                                                                                                                                                          FRAMEWOPK 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT:
                                                                                                                                                        IMMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                                                                                                                                Query Match 46.6%;
Best Local Similarity 60.2%;
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.38;
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hes 60, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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132
147
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119
133
147
147 AA;
                                                                                                                                                                                                                                                                         116 AA;
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                                                           SEQUENCE FROM N A
                                                                      STRAIN-BALB/CJ;
MEDLINE; 89279149.
                                                                                                                                                                                                              54
68
85
40
116
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HV2H_HUMAN
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SEQUENCE
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Query Match 45.1%; Score 4.7; 58 5; Length 137; Best Local Similarity 58.8%; Pred. No. 4.34e-66; Matches 57; Conservative 19; Mismatches 21; Indels
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RESULT
ID HV3
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1 EVQLLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSTIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l, Gaps
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21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PRECUESOP V REGION (MOPC 141)
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                               IG HEAVY CHAÎN PRECURSOR V PEGION (733)
MUS MUSCULUS (MOUSE).
EUKRAYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA: ROBENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG HEAVY CHAIN V REGION (733).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 56.6%; Pred. No. 4.25e-64;
Matches 56; Conservative 22, Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEVY N S , MALIPIERO U.V., LEBECOUE S.G., GEARHART P.J., J. EXP. MED. 169:2007-2019(1989).
PIR; JT0510; HYMS73.
HSSP: P01082; 1BAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 ynpspksrttitrdtskngfflemnsltaedtatyycar 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 npslknrvsitrdtsengfflklnsvttedtatyyca 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 115 BY SIMILARITY.
117 117
117 AA; 13223 MW, 47664D8E CRC32;
                                                                                                                            61 NPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCA 97
                                                                                                                                                                                                                                                      01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 144 AA.
                                                                                                                                                                                                                  PRT;
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117
115
117
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                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 89279149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BALB/CJ;
                                                                                                                                                                                                                  HV62_MOUSE
P18533:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HV43_MOUSE
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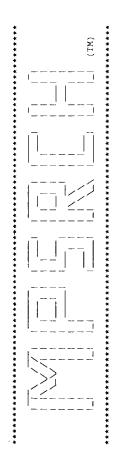
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61 NPSLNDRVF-MSVDRSKDQVSLRLSSVTAADTAVYXCARSPIKMNGRM-MLDAFDIWGGG 119
                                                                                                                                                                                                                                             79 nstlksrltitkdnsksqvflkmnslqtddtaryycasvsi-yyygrsdkyftldywqqg 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 evglgesgpslvkpsgtlsltcsvtgdsi tsdywnwirkfpqnklehmgyisysgstyy 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVOLLESGPGLVKPSGTLSLTCTVSGGSIPSSHWWSWVPOPPGKGLEWIGFVFFSGSTIY 60
                                                                                                                                             1 EVQLLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSTIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.0%; Score 398; DB 5; Length 114;
58.8%; Pred. No. 6.83e-62;
7ative 19; Mismatches 20; Indels 1; Gaps
                                                                                                 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (PRI. 01, LAST ANNOTATION UPDATE)
IG HEAYY CHAIN V REJION (36-60).
IG HEAYY CHAIN V REJION (36-60).
BUTS MISCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METAZGA; CHOPDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
                                         Query Match

8est Local Similarity 53.5%; Pred. No 7 07e-64;
Matches 68; Conservative 26; Mismatches 30; Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE: 82059449.
OLLO R., AUFFRAY G., SIKOPAV G.1., ROUGEON F.;
NINCLEC ACIDS RES 9.4049-4109(1981).
EMBL: V00774; G51651; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A02098; GZMS60.
HSSP, P01825; 1HFM.
IMMUNOGLOBULIN V PEGION; ANTIAPSONATE ANTIRONY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 AA; 12734 MW; F18CE78F CRC32;
144 AA; 15759 MW; 10E3A531 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 npslksrisitrdtskngyylqlnsvtsedtatyyct 96
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21-JUL-1986 (REL. 01, LAST SEQUENCE HPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NPSINDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IG HEAVY CHAIN PPECHPSOR V REGION (441).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 58.88;
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; METAZOA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                    138 tsvtvss 144
                                                                                                                                                                                                                                                                                                                                                                                                  120 TLVIVSS 126
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HV47_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HV36_MOUSE
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       SEQUENCE
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1 e:kllesggglvqpggslklscaasgfdf.skywmswvrqapgkglewigeihpdsgtin 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EVOLLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSTI- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 evkllesgggglvqpggslklscaasgfdf-srywmswvrqapgkglewigeinpdsstin 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVQLLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSTI- 59
                                                                                                                                                                                                                                                                                                                                   Gars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 79223895
MEDLINE; RUDINCHES , KROTZSCH H., POTTER M.:
PROC. NATL. ACAD. SCI. U.S.A. 76-2890-2894(1979).
-i- THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN THAT RINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA: METAZOA: CHOPDATA: VEPTERPATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA, METAZOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA.
EUTHERIA, RODENTIA.
                                                                                                                                    IG HEAVY CHAIN V REGION (441).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
42 8%; Score 396; DB 5; Length 119;
Best Local Similarity 56.6%; Pred. No. 1 88e-61;
Matches 56; Conservative 20; Mismatches 21; Indels
                                                                                                                                                                                                                                                                 DR 5; Length 116
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                20, Mismatches 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 ytpslkdkfiisrdnakntlylqmskvrsedtalyycar 116
                                                                                                                                                                                                                                                              Score 396; DR 5; 1
Pred. No. 1.88e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 YNPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 ytpslkdkfiisrdnakntlylqmskvrsedtalyycar 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 YNPSLNDRVFMSVDKSKDQVSLPLSSVTAADTAVYYCAP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 119 119 119 MW; EEE850E1 CRC32;
                                                                                                 1 18 IS HEAVY CHAIN V 116 116 AA; 12911 MW; 44252075 CRC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (PEL. 01, CPEATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE PRDATE)
21-JUL-1986 (PEL. 01, LAST ANNOTATION UPDATE)
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
HAVY CHAIN V REGION (X44).
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 AA
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                                                                  IMMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                                                                                                     42.88;
                                                                                                                                                                                                                                                                                                    Best Local Similarity 56.6%;
Matches 56, Conservative
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HSSP; P01810; 1FVW.
IMMUNOGLOBULIN V PECION.
PIR; A02076; HVMS44.
HSSP; P01810; 1FVW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 79223895
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119
116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HV38_MOUSE
P01808;
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P01807;
                                                                                                                                                                NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                     Query Match
                                                                                                        SIGNAL
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                                                                                                                                                                                                                    1 EVGLLESGEGLVKPSGILSLICIVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSII- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 42.7%; Score 395; DB 5; Length 119;
Best Local Similarity 55 6%; Pred. No. 3.13e-61;
Matches 55; Conservative 21; Mismatches 21; Indels 2; Gaps
                                                                                                                                                    2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BHAT T.N , NAVIA M A , COHEN G H , PAO D.N , PUDIKOFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA; CHOPDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPOTEINS 1:74-AO(1986)
--- THIS CHAIN WAS ISOLATED FPOW A MYELOWA PROTEIN THAI BINDS
                                                                                                               Score 396; DB 5; Length 119; Pred. No. 1 88e-61; 20; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 79223895.
PAO D.N., PUDIKOFF S., KRUTZSCH H., POTTER M.;
PROC. NATL. ACAD. SCI. U.S. A. 76·2890-2894(1979).
                                                                                                                                                                                                                                                                         60 ytpslkdkfiisrdnakntlylqmskvrsedtalyycar 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116
13240 MW: 6892320D CRC32;
                                                                 NON_TER 119 119 119 SEQUENCE 119 AA: 13246 MW; Alceb710 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                        . LAST SEQUENCE UPDATE)
. LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A02080; AVMSJ5.
PDB; 2FBJ; 15-0CT-90.
IMMUNOGLOBULIN V PECION; 3D-STPUCTUPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-PAY CPYSTALLOGPAPHY (2 A ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                     21-701-1986 (REL. 01, CREATED)
21-701-1986 (PEL. 01, LAST SEQ
01-MAP-1992 (PEL. 21, LAST ANW
IG HEAVY CHAIN V PEGION (J539)
                                                                                                                 Query Match
Best Local Similarity 56.6%;
Matches 56; Conservative
GALACTAN.
PIR; A02077; AVMSX4.
HSSP; P01810; 2FBJ.
IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 88217852.
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                                                                                                                                                                                                                                                                                                                                        LI 14
HV40_MOUSE
P01810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAVIES D.R.;
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STRAND
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1 evkllesggglvqpggslklscaasgfdf-sgywmswvrqapgkglewigeinpdsstin 59
                                                                                                                                                                                                                                                                                                                                                             2; Gaps
1 EVQLLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSTI- 59
                                                                                                                                                                                    HV41_MOUSE STANDARD; PRT; 117 AA.
P01811;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
1G HEAVY CHAIN V REGION (UPC10).
MUS MUSCULUS (MOUSE).
BUKARYOTA; METAZOA CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 54.0%; Pred. No. 2.97e-59;
Matches 54; Conservative 23; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                            60 ytpflkdkfiisrdnakntlflqmskvrsedtalyfcarn 99
                                                                                                                                                                                                                                                                                                                                                                                                       60 ytpslkdkfiisrdnaknslylqmskvrsedtalyycar 98
                                 Search completed: Tue Feb 24 07:13:38 1998 Job time : 16 secs.
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Pelease 2.1p John F. Collins, Riccomputing Pescarch Unit Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Peb 24 07-41-10 1999; MasPar time 3.35 Seconds 191.725 Million cell updates/sec Pun on:

Tabular output not generated.

Description: Perfect Score:

. PMMLDAFDIWGQGTLVIVSS 126 >US-08-844-215-6 (1-126) from US08844215.pep 925 I EVQLLESGPGLVKPSGTLSL Sedneuce.

PAM 150 Gap 11 Scoring table:

56402 seqs, 5095871 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-issued libackl 2:51 3:52 4:53 5:54 6 55 7:56 8 PCT90 9.PCT91 l0.PCT92 11:PCT93 12:PCT94 12:PCT97 14 PCT96 Mean 28.331; Variance 154.255; scale 0.184 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	.31e-33	.78e-33	786-33	.28e-31	.25e-30	.56e-30	470-29	.95e-29	.96e-29	62-096	200-29	.98e-27	.75e-27	740-27	740-27	026-27	.29e-26	250-25	486-25	.48e-26	100	5400-24
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Description	Sequence	Sequence	Sednence	Sequence	Sequence	Sequence	Seguence	Sequence						Sequence						Sequence	Segmente	Sequence
ID	US-08-478-	PCT-US95-0	US-08-276-	- 1	8	US-08-478-	80	78-08-111-	PCT-US93-0	US-08-211-	P <u>r</u> T-13893-1	US-08-478-	US-08-478-	18-08-468-	ris-n8-259-	US-08-478-	PCT-US95-1	US-07-942-	US-08-467-	US-08-470-	PCT-9293-1	US-08-211-
DB	7	13	7	۲-	7	7	۲-	(°)	11	ŀ	드	7	7	۲-	Œ	1	13	^	۲-	۲-	Ξ.	۲-
% Query Match Length	86	126	126	125	121	139	121	001	120	120	110	124	119	134	134	116	119	107	119	119	129	77 F7
% Query Match	60.4	•	σ.	57.6	56.2	55.0	54.7	54.3	54.3	54.3	54.1	51.7	51.1	50.9	50.9	50.8	50.2	6	49.6	49.6	48.1	47.2
Score	559	553	553	533	520	509	206	502	502	502	500	478	473	471	471	470	464	462	459	459	445	437
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23 437 47.2 114 11 PTT US93-5 Sequence 23, Applicatic 2.540-24 437 47.2 114 6 US-08-111- Sequence 23, Applicatic 2.540-24 420 45.4 147 7 US-08-159- Sequence 3, Applicatic 4.900-23 412 44.9 110 7 US-08-159- Sequence 18, Applicatic 4.900-23 28 412 44.9 120 11 PCT US93-1 Sequence 18, Applicatic 1.950- 129 411 44.4 134 10 PCT US93-1 Sequence 17, Applicatic 1.950- 129 411 44.4 134 7 US-08-111- Sequence 16, Applicatic 2.340-22 31 411 44.4 134 7 US-08-111- Sequence 16, Applicatic 2.340-22 31 411 44.4 134 7 US-08-111- Sequence 16, Applicatic 2.340-22 31 411 44.4 134 11 PCT-US93-1 Sequence 16, Applicatic 2.340-22 31 411 44.4 134 11 PCT-US93-0 Sequence 16, Applicatic 2.340-22 31 411 44.3 119 7 US-08-11- Sequence 16, Applicatic 2.780-22 410 44.3 119 7 US-08-20- Sequence 19, Applicatic 2.780-22 410 44.3 119 7 US-08-20- Sequence 19, Applicatic 2.780-22 41 41 41 41 41 41 41 41 41 41 41 41 41	US-08-478-039-75 STANDARD, P XXXXXX 01-JAN-1900 Sequence 75, Application US/08478039 Fatent No. 568122 GENERAL INFORMATION. POTOMICANT: Newmen, Roland A. APPLICANT: Newmen, Roland A. APPLICANT: Newmen, Roland A. APPLICANT: Newmen, Potomorphinant NUMBER OF SEQUENCES: 114 ADDRESSEE: RUPNS, DOANE, SWEC STREET: QS PRINCE SE. CITY: Alexandria STATE: VA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: WAS COUNTRY: WAS COUNTRY: PREABABLE FORM: MEDIUM TYPE: FLORPY disk COMPUTER PRADABLE FORM: MEDIUM TYPE: FLORPY disk COMPUTER PRADABLE FORM: APPLICATION NUMBER: US/08/478 FILING DATE: 10-JUL-1995 PRIOR PAPICATION NUMBER: US OT/856 FILING DATE: 25-JAN-1995 PRIOR APPLICATION NUMBER: US OT/856 FILING DATE: 25-JAN-1995 PRIOR DATE: 25-JAN-1995 PRIOR APPLICATION NUMBER: US OT/856 FILING DATE: 25-JUL-1991
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STATE:
                                              119 VSS 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LLESGPGL*KPSETLSLTCTVSGGSLSSFDW-NWIRQPAGKGLEWIGRIYPSGNTHYNPS 59
                                                                                                                                                                                                                         1 QVQLQESGPGLVKPSETLSLTCAVSGGSISSSYYWSWIRQPPGKGLEWIGYIYYSGSTYY 60
                                                                                                                                                                                                                                      D, Caps
                                                                                                                                                                                                        O, Gups
                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS NUMBER OF SEQUENCES: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OMFUTER: FLORPY disk
COMFUTER: FLORPY disk
COMFUTER: IBM PC compatible
COMFUTER: DATE: PC-DOS/MS-LOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 553; DB 13; Length 126;
Pred. No. 3.78e-33;
14; Mismatches 25, Indels
                                                                                                                                                                                    Score 559; DB 7; Length 98; Pred. No. 1.31e-33;
                                                                                                                                                                                                       10; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                           126 AA.
                                                                                                                                                                                                                                                                                    61 NPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCAR 98
                                                                                                                                                                                                                                                                  61 NPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR 98
                     012712-160
                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 142:
                                                                                                                                       ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH4 consensus
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 142, Application PC/TUS9508743
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 142, Application PC/TUS9508743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE. protein
JENCE 126 AA, 13684 MW, 88548 CN;
                                                                                                                                                                     98 AA; 10732 MW; 59041 CN;
NAME: Teskin Esq., Robin L. REGISTRATION NUMBER: 35,030 REPERROLE/DOCKET NUMBER: 012 TELECOMMUNICATION INFORMATION: 703-836-6620
                                                                                                SS: not relevant not relevant
                                                          INFORMATION FOR SEQ ID NO: 75: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 126 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                               LENGIH: 98 amino acids
                                   TELEPHONE: 703 cc.
TELEPHONE: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.88;
66.78;
                                                                                                                      peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                  Query Match
Best Local Similarity 78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7.,
82; Conservative
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                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                               SOURCE:
                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                           PCT-US95-08743-142
                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
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60 LESEVTMSRDISKNOFSVKLISVTAADIALYYCARENIGRITEEIG-NFFDIWGGGILVI 118
                           64 INDRVEMSVDKSKDQVSLRLSSVTAADTAVYYCARSPIKMNGGRMALDAFDIWGGGLIVI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LLESGPGLVKPSETLSLTCTVSGGSLSSFDW-NWIROPAGKGLEWIGRIYPSGNTHYNPS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Mismatches 25; Indels 2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lerner, Richard A TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIRODIES TITLE OF INVENTION: TO HUMAN IMMUNOBEFICIENCY VIRUS NUMBER OF SEQUENCES: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 16666 No 5652138th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Condition 59.8%; Score 553; DR 7; Length 126; Local Similarity 66.7%; Pred No. 3.78e-33; les 82; Conservative 14. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,148
                                                                                                                                                                                                                             PPT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
JENCE 125 AA; 13684 MW; 88548 CN;
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 142, Application US/08276852
Patent No. 5652138
GENEPAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             Sequence 142, Application US/08276852.
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TELECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 142:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dennis R
Carlos F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-SEP-1992
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                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Fitting, Thomas REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burton,
Barbas,
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                                                                                                                                                                                                                               US-08-276-852-142
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CA
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4 LLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSTIYNPS 63
                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Recombinant Antibodies for Human Therapy NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1 0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NOTE: US/08/478,039 FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                  125 AA
                                                                                                                                                                                                                                                                                                 STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Teskin Esq., Robin L
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
FRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
                                                                                                                                  PPT.
                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                       Sequence 76, Application US/08478039
Patent No. 5681722
GENERAL INFORMATION:
APPLICANT: Hanna, Roland A
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W
                                                                                                                                                                                                   Sequence 76, Application US/08478039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SS: not relevant not relevant
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TELEPAX: 703-836-2021
INFORMATION FOR SFQ. ID NO: 76-
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 amino acids
                                                                                                                                  STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide OPIGINAL SOURCE.
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER PEADARLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Monkey
                                                                                                                                                                                                                                                                                                                                                                                  22313-1404
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                                                                                                                                 US-08-478-039-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                119 VSS 121
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61 YNPSLKNRVIISVDISNNQFSLKMISVIAADTAIYYCARGDVI-S-GWYR-GYFDSWGQG 117
                                                                                                                                                                               60 YNPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCARSPIKMNQGRMMLDAFDIWGQG 119
                                                                                              1 QMQLQESGPGLVKPSETLSLTCAVSGGSISSSYDWTWIRQPPGMGLEWIAVISGNSGSAD 60
                                                                                                                         1 EVOLLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVF-FSGSTI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Hanna, Nabil
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
                            Score 533, DB 7, Length 120;
Pred No. 1.29e-31;
"...martches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERALING SYSTAM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pelease #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: BURNS, DOANE, SWECKER & MATHIS 699 Prince St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEPEPENCE/POCKET NUMBER: 012712-160
TELEFORMUNICATION INFORMATION:
TELEPHONE: 703-836-6520
TELEFAX: 703-836-2021
 VH4 clone 4-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/379,072 FILING DATE: 25-7AN-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/912,292 FILING DATE: 10-30L-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                             PRT;
CHROMOSOME/SEGMENT: VH4 clone 4
VCE 125 AA; 13363 MW; 90929 CN;
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 80, Application US/08478039 Patent No. 5681722 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              Sequence 80, Application US/08478039.
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ATTORNEY/AGENT INFORMATION:
NAME: TESKIN ESG, POPIN:
REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                             STANDARD;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COPPESPONDENCE ADDRESS:
                                       57.6%,
Local Similarity 63.0%;
les 80; Conservative
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CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                           US-08-478-039-80
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                                                                                                                                                                                                           118 CLVTVSS 124
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             SEQUENCE
                                         Query Match
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                                                                     Matches
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61 YNPSLNNRVSISIDTSKNLFSLKLRSVTAADTAVYYCASNILKYLH-WL-L--Y--WGQG 114
                                                                                                                                                                                                                                     1 QVQLQEAGPGLVKPSETLSLTCSVSGGSISGDYYWFWIRQPPGKGLEWIGYIYGSGGGTN 60
                                                                                                                                                                                           7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                Score 520, DB 7; Length 121;
Pred. No. 1.25e-30:
19; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSEE: BURNS, DOANE, SWECKER & MATHIS : 699 Prince St. Alexandria
                                                                                                 CHROMOSOME/SEGMENT: VH4 anti-CD4 CHIM ICE 121 AA; 13232 MW; 88649 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-708/478,039
07-708-1995
N: 435
                                                                                                                                                                                                                                                                                                                                            PRT;
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APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER: US 07/912,292
10-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER: US 07/856,281
23-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US 07/735,064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 108, Application US/08478039
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 108, Application US/08478039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Newman, Roland A. APPLICANT: Hanna, Nabil APPLICANT: Raab, Ronald W.
                       TOPOLOGY: not relevant MOLECULE TYPE: pential ORIGINAL
                                                                                                                                                                                                                                                                                                                                               STANDARD;
         : 121 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 23-MAR-1
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SEQUENCE CHAPACTEPISTICS:
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                                                                                                                                     Match
Local Similarity 63.0%;
les 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                             ORGANISM: Monkey POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5681722
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                               US-08-478-039-108
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             LENGIH:
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                                                                                                                 SEQUENCE
                                                                                                                                       Query Match
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                                                                                                                                                               Matches
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TITLE OF INVENTION: Recombinant human anti-human immunodeficiency TITLE OF INVENTION: virus antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 YNPSLNNRVSISIDTSKNLFSLKLRSVIAADTAVYYCASNILKYLH-WL-L--Y--WGOG 133
                                                                                                                                                                                                                                                                                                                     60 YNDSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCARSPIKMNOGRMMLDAFDIWGGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 65.4%; Pred. No. 1.47e-29;
Matches 83; Conservative 12; Mismatches 25; Indels 7; Gaps
                                                                                                                                                                                                                                                    20 QVQLQEAGPGLVKPSETLSLTCSVSGGSISGDYYWFWIRQSPGKGLEWIGYIYGSGGGTN 79
                                                                                                                                                                                                                                                                  7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/275,053
                                                                                                                                                                                                    55.0%; Score 509; DB 7; Length 139; 61.9%; Pred. No. 8.66e-30;
                                                                                                                                                                                                                             20; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          121 AA.
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PRIOR APPLICATION DATA:
                                               012712-160
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MEDIUM TYPE: Floppy disk
COMPUTER: PR PR COMPATIBLE
COMPUTER: IB PR COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
SEQUENCE 121 AA; 13365 MW; 86912 CN;
                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 139 AA; 15445 MW; 115855 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/08275053
Patent No. 5607847
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/08275053.
                                      35,030
                                                REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                           TELEFAX: 703-836-2021 INFORMATION FOR SEQ ID NO: 108:
                        NAME: Teskin Esq., Robin L. REGISTRATION NUMBER 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 121 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFOPMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                139 amino acids
                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                     Dest Local Similarity 61.9%;
Matches 78, Conservative
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                                                                                                                                           amino acid
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                                                                                                                                LENGTH:
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1 EVQLLESGPGLVKPSGILSLTCIVSGGSIRSSHW-WSWVRQPPGKGLEWIGEVFFSGSTI 59

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60 YNPSLNDPVFMSVDKSKPQVSLPLSSVTAADTAVYYCAPSPTKMNGGRMMLDAFDIWGGG 119
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Pred. No. 2.966-29;
12; Mismatches 25; Indels 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE. Patentin Pelease #1.0, Version #1 25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: HIV Immunotherapeutics NUMBER OF SEQUENCES: 38 COPPESSONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT/US92/07111
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PCLASSIFICATION: 424
PCLASSIFICATION DATA
APPLICATION NUMBEP 98 07,748,562
FILING DATE: 22-A00-1991
PRIOR APPLICATION DATA
APPLICATION NUMBER: PCT/US92/07111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APP-1993
ATTORNEY/AGENT INFOPMATION:
                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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JENCE 120 AA; 13278 MW; 84976 CN;
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REFERENCE/DOCKET NUMBER: 316
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 24-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
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                                                                                                                                                                                                                                                                        STANDAPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 5558865
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
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Local Similarity 65.1%;
nes 82; Conservative
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CITY: Chicago
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120 TLVIVSS 126
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TOPOLOGY:
                                                                                                         115 SLVTVSS 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 502; DB 11; Length 120;
Fred. No. 2.95e-29,
12; Mismatches 25, Indels 7; Gaps
                                                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Falease #1 0, Version #1.25 CURPENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07967
                                                                                                                                                                                                                  6300 Sears Tower, 233 S Wacker Drive
          120 AA.
                                                                                                                                                     TITLE OF INVENTION: HIV Immunotherapeutics
NUMBER OF SEQUENCES: 38
CORPESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER. FCI/US92/07111
PILING DATE. 24.70G.1992
PRIOR APPLICATION DATA:
            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US 08/039,457
                                                                                                               Sequence 28, Application PC/TUS9307967
GENERAL INFORMATION-
APPLICANT: Ohno, Tsuneya
                                                                                      Sequence 28, Application PC/TUS9307967.
                                                                                                                                                                                                                                                                                    COMPUTER PEACABLE FORM:
MDDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-FOS/WS-FOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
JENCE 120 AA; 13278 MW; 84976 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Borun, Michael F. REGISTRATION NUMBER: 25,447 PEPEPENCE/DOCKET NUMBEP: 314 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (312) 474-520
TELEFAX. (322) 474-5448
TELEX: 25-3856
INFOPMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 22-APR-1993
ATTORNEY/AGENT INFORMATION:
            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
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Best Local Similarity 65.18,
Matches 82, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                     COUNTRY: HEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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CITY: Chicago
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          PCT-US93-07967-28
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                                                             01-JAN-1900
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Patentin Release #1.0, Version #1.25
                                                                                              119 AA.
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1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT/US93/10555
                                                                                                PRT;
                                                                                                                                                                                                               Sequence 16, Application PC/TUS9310555 GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TILLE OF INVENTION. METHOD FOR STIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 AA; 13135 MW; 76375 CN;
                                                                                                                                                                                  Sequence 16, Application PC/TUS9310555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: HOWELLS, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFOPMATION FOP SPQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-OCT-1993
                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S4.18;
Local Similarity 62.58;
es 75; Conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER PEADABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                              Los Angeles
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                              TITLE OF INVENTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                              PCT-US93-10555-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                          90067
                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
         115 SLVTVS 120
                                       120 TLVIVS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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                                                                                                                                                            01-JAN-1900
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                                                                                                                                 XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YSPSIKSKVTMLRDTSKNQFSLRLSSVTAADTAVYYCARE----NHG-TT-TSMDYWGQG 114
1 QVQLQESGPGLVRPSQTLSLTCTVSGFSITSSSYCWHWVRQPPGRGLEWIGRICYEGSID bU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVOLLESGPGLVKPSGTLSLTCTVSGGSIRSSHW-WSWVRQPPGKGLEWIGEVFFSGSTI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 502; DB 7; Length 120; Pred. No. 2.96e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25; indels
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTLM Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,980
                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago
                                                                                                                                      120 AA.
                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HIV Immunotherapeutics NUMBER OF SEQUENCES: 38 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07111
FILING DATE: 24-AUG 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,457
FILING DATE: 22-APR 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
FENCE 120 AA; 13278 MW; 84976 CN;
                                                                                                                                                                                                                                                    Sequence 28, Application US/08211980
Patent No 5665569
                                                                                                                                                                                                                             Sequence 28, Application US/08211980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 31t
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25,447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 28:
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amino acid
                                                                                                                                         STANDAPD;
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                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 54.3%;
Best Local Similarity 65.1%;
Matches 82, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
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                                                                                                                                         US-08-211-980-28
                                                  115 SLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                             120 TLVIVS 125
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METHOD FOR STIMULATING PRODUCTION OF VARIABLE REGION GENE FAMILY PESTPICTED ANTIBODIES
                                                                       TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 NPSLISRVIMSLDISKNQFSLKLISVIAADIAVYYCARGPCEAYCTDDAPOAYFGHWGOG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQQWGAGLLKFSETLSLTCAVYGGPF-SGYYWSWVPQPPGKGPFWIGEINHSGRTTY 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Mismatches 27; Indels 2: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 500; DB 11; Length 119;
Pred, No. 4 20e-29;
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1 EVQLLESGPGLVKPSGTLSLTCTVSGGSIRSS-HWWSWVRQPPGKGLEWIGEVFFSG-ST 58

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TITLE OF INVENTION: Recombinant Antibodies for Human Therapy NUMBER OF SEQUENCES: 114 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 478; DB 7; Length 124;
Pred. No. 1.98e-27;
14; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/379,072
FILING DATE: 05-JAN-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/312,23
FILING DATE: 10-JUL-1992
PRIOR APPLICATION NUMBER: US 07/312,23
FILING DATE: 10-JUL-1992
PRIOR APPLICATION NUMBER: US 07/7856,281
APPLICATION NUMBER: US 07/7856,281
            124 AA.
                                                                                                                                                                                                               ADDRESSEF. BURNS, POANE, SWECKER & MATHIS STREET: 699 Prince St. CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 703-836-6520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH4 clone 4-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735.064
FILING DATE: 25-771-1991
ATTORNEY/AGENT INFORMATION:
           PFT;
                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 AA; 13147 MW; 95091 CN;
                                                                                                        Sequence 78, Application US/08478039
Patent No 5681722
                                                                                 Sequence 78, Application US/08478039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS: not relevant not relevant
                                                                                                                                          APPLICANT: Newman, Roland A. APPLICANT: Hanna, Nabil APPLICANT: Raab, Ronald W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 78:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 amino acids
            STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 62.5%;
Matches 80; Conservative
                                                                                                                                                                                                                                                                                     COMPUTER READARLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 22313-1404
                                                                                                                  Patent No 5681722
GENERAL INFORMATION:
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          US-08-478-039-78
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                                                                                                                                                                                                                                                    STATE:
                                                          01-JAN-1900
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                                    XXXXXX
RESULT
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1 QVHLQESGPGLVKPSETLSLTCSVSGSISSSGYYWGWIPQPPGKGLEWIGSIHGSGRSN 50

7; Gaps

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59 IYNPSLNDPVEMSVFKSKKKVVSLPLSSVTAAETAVYYGAFSPTKNNQGFMKINAFDIMGQ 118
  61 SLNPSLKSRVTLSVDTSGNKFSLKLSSVTAADTAVYFCARE---LYSSSPYY--FDFWGQ 115
                                                                                                                                                                                                                                                                    APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
AFFLICANT: Raab, Ponald W.
TITLE OF INVENTION: Percombinant Antibodies for Human Therapy
COPPESPONDENCE: 114
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: THE POCHOS/MS-FUGS
OFTWARE: PatentI: Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039
FILING PATE: 07-JUN-1995
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US n8/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION NUMBER: US 08/379,072
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
PRIOR APPLICATION DATA:
                                                                                                                                119 AA
                                                                                                                                                                                                                                                                                                                                                       ADDPESSEE. RUPNS, FOANE, SWECKER & MATHIS STREET: 599 Prince St. CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
                                                                                                                                PPT;
                                                                                                                                                                                                                                   Sequence 77, Application US/08478039
Patent No. 5681722
GENERAL INFORMATION:
                                                                                                                                                                                                           Sequence 77, Application US/08478039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN ESQ., RObin L.
PEGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
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                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPGANISM: Monkey
                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIF: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POSITION IN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                     116 GVRVTVSS 123
                                                                            119 GTLVIVSS 126
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                                                                                                                               US-08-478-039-77
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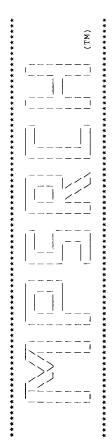
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                                                                                                                                                                                                                                                                                                                                  PRODUCTION OF HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR HEDATITIS B SUPFACE ANTIG
                                                                               1 QVQLOESGPGLVKPSETLSLTCAVSGGSISSGYYWGWIRQTPGKGLEWIGSLQGPGGNKY 60
                                                                                                     1 EVOLLESGPGLVKPSGTLSLTCTVSGGSIRSSHWMSWVRQPPGKGLEWIGEVFFSGSTIY 60
                                   Length 119;
                                   Query Match
Best Local Similarity 68.7%; Pred. No. 4.75e-27;
Matches 68; Conservative 11; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,671
FILING DATE: 06-7110.
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Twomsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                               61 INLCLKSRVTLSADTSKNOFSLKLSSVTAADTAVYYCAR 99
                                                                                                                                             NAME: Smith, William M. REGISTRATION NUMBER: 30,223 REFERENCE/DOCKET NUMBER: 11823-50-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/259,372
FILING DATE: 14 JUN-1994
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US 06/904,517
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      VH4 clone 4-14
                                                                                                                                                                                                      PRT;
         CHROMOSOME/SEGMENT: VH4 clone 4:

ACE 119 AA; 12636 MW; 81453 CN;
                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08468671
                                                                                                                                                                                                                                                                     Sequence 6, Application US/08468671.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
FILLY
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                    WERAL INFORMATION:
APPLICANT: OSLDERG.
ATTLE OF INVENTION: PRODUCT
TITLE OF INVENTION: ANTIBOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 15-JUN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER
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                                                                                                                                                                                                                                                                                                           Patent No. 5648077
                                                                                                                                                                                               T 14
US-08-468-671-6
                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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                      SEQUENCE
                                            Query Match
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ANTIHODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIG
                                                                                                                                                                                                                                 20 QVQLQESGPGLVKAAETLSLTCTVSRGSF-SDYFWNWFRQPAGKRLEWLGRVYTSGSVDY 78
                                                                                                                                                         Length 134;
                                                                                                                                                       Ouery Match 50.9%; Score 471; DB 7; Length 134 Best Local Similarity 69.7%; Pred. No. 6.74e-27; Matches 69; Conservative 11; Mismatches 18; Indels Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ostberg, Lars G. TILLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL TITLE OF INVENTION: ANTIHODIES SPECIFIC FOR HEPATITITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PUCLUS/MS-LOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CUPPENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,372A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                            79 NPSLKSRVTVSVDTSKKQFSLRLSSVTVADTAVYYCARG 117
                                                                                                                                                                                                                                                                                                14-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION
FILING DATE: 14-JUN 17-2
FILING DATE: 14-JUN 17-2
FILING DATE: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,426
APPLICATION NUMBER: US 07/871,426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 21-APP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US U7/576,036
FILING DATE
PRIOR DATE
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          us 06/425,196
                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                  MOLECULE TYPE. protein
JENCE 134 AA; 14995 MW; 109187 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08259372A
Patent No. 5565364
GENERAL INFORMATION:
APPLICANT: Ostberg, Lars G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08259372A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAY-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-0CT-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-1990
         TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                        STANDARD:
                                                                           134 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 11-MAY-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 31-0CT-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                          amino acid
                                                                                                         inear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                               T 15
US-08-259-372A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                         TOPOLOGY:
                                                                              LENGTH:
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                                                                                         TYPE:
                                                                                                                                      SEQUENCE
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Search completed: Tue Feb 24 07:41:23 1998 Job time : 13 secs.

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Release 2.1D John F. Collins, Biccomputing Pescarch Vait. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Pab 24 07:14:35 1998; MasPar timo 6.79 Seconds 257.613 Million cell updates/sec Run on.

>US-08-844-215-6 (1-125) from US08844215.pep 925

Fabular output not generated.

.. PMMLDAFDIWGQGTLVIVSS 126 1 EVOLLESGPGLVKPSGTLSL. Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

111726 seqs, 13889129 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseg30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9.part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part10 21:part11 21:part119 20:part10 21:part21 21:part21 22:part19 21:part23 Mean 30.712; Variance 168.307; scale 0.182 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1111	00000000000000000000000000000000000000	401464444444444444444444444444444444444	100000000000000000000000000000000000000	MARA MARA	Description Human lung cancer spe- F105 rearranged varia Human immunoglobulin Human gern-line gene Anti-human RhD F0G-1 Anti-human RhD F0G-7 Anti-human RhD F0G-1 Anti-human RhD F0G-1 Anti-human RhD All III9, Vh 71-4. Vh 71-4. Vh 71-4. Human immunoglobulin Human immunoglobulin	01144444444444444444444444444444444444
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	589.11.2 589.11.2 58.2	238862 23862 23862 23862	3 C 4 C C C C	W.45454 R865329 R865329 R865298 R26014	Influciolocular inebs/ Human immunoqlobulin MAb 1-3-1 variable re Human immunoqlobulin pfG-RVh-PM1f-4 FYG-RVh-PM1f-4	

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736-3	.20e-3	.20e-3	.20e-3	.11e-3	5 240-30	240-3	.23e-3	410-3	.50e-2	C-086.	3.540-29	.54e-2	54e-2	016-2	000-2	.69e-2	39e-2	.78e-2	.68e-2	.14e-2	.91e-2	.91e-2	.08e-2	1.53e-26
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ALIGNMENTS

			:;
T 1 W06474 standard; Protein; 124 AA. W06474. W06474. W0647. Human lung cancer specific antibody heavy chain variable region Heavy chain; light chain; variable region; human; monoclonal antibody lung cancer issue; diagnosis; purification; cancer-specific antigen; Homo saciens.	Key Incation/Qualifiers //abel- CDRI //abel- CDRI //abel- CDRI //abel- CDRI //abel- CDR2 //abel- CDRI //abel- CDR3 //ab	therapy	î, Gaps
ole reg octonal	olls :	logical	4
varjak n; mond ncer-sp	r cancer cells - also or for purification the heavy chain and hal antibody which is	immuso is.	
/ chain n; huma ion; ca	tung ca er, or te the	e, for antige	DB 20; .59e-37; cles 21,
y heavy region ificat:	human ce cance	cancer ecific	10 . 1
24 AA. antibod ariable is; pur	alifier ive to diagnos sc. 74-75 r a huma a huma cor tiss	mosis of cancers, for im cancer-specific antigen.	Score 618; Pred. No. 1 13, Mismut
14 standard; Protein; 124 AA. 44. 17- 17- 17- 17- 17- 17- 17- 17- 17- 17-	Redion /label= CDR1 /label= CDR1 /label= CDR2 /label= CDR2 /label= CDR2 /label= CDR2 /label= CDR2 /label= CDR3 /label= CDR	he used for clinical diagnosis of cancers, for immunological or for purification of a cancer-specific antigen. Sequence 124 AA;	66.8%; 71.4%; ative
d, Pro first cer sp ight c	Location 131.36 131.36 51.66 51.66 7, Claim 97 99.103 7, Claim 97	clinical fication 124 AA;	66.8% Similarity 71.4% 90; Conservative
14 standar 4; 1997 (1 lung car cancer ti sapiens.	CDR1 CDR2 CDR3 CDR3 CDR3 CDR3 CDR3 CDR3 CDR3 CDR3 TQR4849 TQR849 TAPECIF CONDING D SPECIFIC SPECIFIC SPECIFIC TOTAL SPECIFIC SPE	for cl purific e 124	h Simila 90; C
M06474 standard; Protein; W06474 standard; Protein; 23-MAY-1997 (first entry) Human lung cancer specific Heavy chain; light chain; Hung cancer tissue; diagno Homo sapiens.	Regy 1000 1000 1000 1000 1000 1000 1000 10	be used for clinical di or for purification of Sequence 124 AA;	Query Match Best Local Similarity 71.4%; Matches 90; Conservative
RESULT ID W AC AC DT 2 DT 2 DE H KW H KW 1		5558	Que: Best Matt

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F105 rearranged variable region heavy chain.
Monoclonal antibody: MAb; envelope; glycoprotein; gp120; HIV; AIDS;
CD4; receptor, hybridoma; polymerase chain reaction, FCR, heavy, light;
                                                                        61 NPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCARSPIKMNQGRMMLDAFDIWGQGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            monitoring HIV infection
Claim 9-10; Page 77: 109pp: English.

Claim 9-10; Page 77: 109pp: English.

MRNA from the known hybridoms F105 was converted to cDNA and this subjected to PCK amplification using primers corresp. to appropriate parts of the heavy or light chains and having restriction sites to permit cloning. The extension prods. were isolated and sequenced. The recombinant human moncolonal antibody (MAb) binds to a discontinuous epitope on the HIV gpl20 envelope glycoprotein, blocks the binding of gpl20 to the CDA receptor, and neutralises a broad deficiency, esp at doses of 0.1-10 mg/kg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 spslksrvtisvetsknqfslkltsmtaadtavyycargpvpavfygdyrldp----wqqg 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NPSLNDRVFWSVDKSKDQVSLRLSSV1AAD/TAVYYCAKSPIK-MNGSRMMLDAFDIWGGG 119
61 nps1ksrvtisadtsknqfs1kvnsvtaadtavyycarrnydfwsggd--gpfdywqggt 118
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Human immunoglobulin variable heavy chain #26.
Primer: PCP: amplify: human: immunoglobulin; variable; heavy chain; cosmid; piacenta; vector; pJB81; E.coli; mammalian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA segments encoding monoclonal antibody - which binds to gpl20 and neutralises HIV, for treating ALDS, and for diagnosing and
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(NEWE-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chain; epitope; immune deficiency.
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                                                                                                                                                                                                                                                                                                                                                                R41285 standard, Protein; 142 AA. R41285,
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Best Local Similarity 68.5%;
Matches 87; Conservative
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10-DEC-1991; US-804652.
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Protein 20..
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Sequence 142 AA;
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WPI; 93-214174/26.
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WO9426895-A.
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production of human immunoglobulin in mammalian hosts

Disclosure; Page 67-68; 130pp; Japanese.

Disclosure; Page 67-69; 130pp; Page 67-69; 130pp; Page 67-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVOLLESGPGLVKPEGILSLICIVSGGSIPSSHWWSWVPQPPGKGIFWIGEVFFSGSTIY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-FEB-1994 (first entry)
Human germ-line gene DP-68/JH6 antibody heavy chain.
humanised antibody; human germ-line; heavy chain; variable region;
framework region, reshaped antibody. CDE grafted antibody;
                                                                                                                                                                                  DNA fragment comprising human immunoglobulin Vh genes - for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 567; DR 12; Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 4.15e-33;
11; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 77.6%;
Matches 76; Conservative
                                                                         (NISB) JAPAN TOBACCO INC.
Honjo T, Matsuda F;
WPI; 95-006791/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label = FR1
/note= "framework region"
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19-FEB-1992; GB-003459.
(SCOT-) SCOTGEN LTD.
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24-NOV-1994.
10-MAY-1993; J00603.
10-MAY-1943; WO-J00603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51..66
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                                                                                                                                                          N-PSNR; 078966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label - CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label- CDR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= FR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label= FR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carr FJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding complementary determining regions - of human anti-rhesus D antibodies, useful in prodn. of monoclonal antibodies and for passive immunisation
Disclosure, Fig 5, 32pp; English.

The DNA sequence of eleven monoclonal antibodies are represented in 019145-57. Synthetic genes, for both heavy and light chains may be created by combining selected CDR 1, 2, and 3 regions, which may be selected from different antibody mols. having varied binding specificity. The chimaeric anti-rho antibodies can be used for diagnosis and therapy, and are capable of providing blood-typing reagents of high specificity and reclability. They can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sing reagents of high specificity and reliability. They can also used in passive immunisation to prevent haemolytic disease of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 qvqlqesgpglvkpsdtlsltcavsgysisssnwwgwirqppgkglewigyiyysgstyy 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVQLLESGPGLVKPSGTLSLTGTVSGGSIPSSHWWSWVPQPPPGKGLEWIGFVFFSGSTIY 60
                                                                                                                           A humanised antibody comprised CDPs criginally from a mouse MAD RSV19 specific for Respiratory Syncytial Virus transplanted onto heavy and light chain V region domains derived from NEWA and REI myeloma proteins, respectively. The framework regions of this CDP-grafted antibody were converted to the germ-line equivalent For conversion of the H-chain, the germ-line heavy chain DeF68/H6 (R4093) was used Germ-line framework regions are those present in mmature B cells, i.e. prior to any somatic mutation which takes place during maturation. Unlike mutations in the CDRs, any mutation place during maturation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                           in framework regions does not affect affinity for an antigen and is therefore essentially random. The mutation may, however, cause the "self" antibody to be recognised as "foreign" and conversion to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                              unmutated germiline sequence renders the framework regions "immuna
                       New altered antibodies with reduced immune responses - have germ-line aminoacid residues replacing somatically mutated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 567, DB 8, Length 117.
Pred. No. 4.15e-33;
11; Mismatches 11; Indels
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Monoclonal antibody, rhesus D; blood-typing; CDR:
haemolytic disease of the newborn; HDN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 npslksrvtmsvdtsknqfslklssvtavdtavyycar 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                       Example 3; Fig 4a; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P12266 standard: Protein; 124 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BLOO-) CENT BLOOD LAB AUTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 61.3%.
Best Local Similarity 77.6%;
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hughes- Jones N;
WPI; 91-178104/24
WPI: 93-288411/36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label - CDR3
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varied binding specificity. The chimaeric anti-shib antibodies can be used for diagnosis and therapy, and are capable of providing blood-typing reagents of high specificity and reliability. They can also
                                                                                                                                                                                                60 npslrsrvtisydtsknqfslklgsvtaadtavyycarvlysrtisqysy-ymdvwgkgt 118
                                                                                                                                                                                                                                                   61 NPSENDPVFMSVDKSKDDVSEPESSVTAADTAVYYCAPSPIKMNGGRMMEDAFDIWGQGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 qvqlqesgpglvkpsetlsvtctvsggsvsssyw-swirqppgkgpewigyiyysgstny 59
                                                                                                                                     1 EV_LLESGPGLVKPSGTLSLICIVSGGSLHSSHWWSWVPQPPGKGLEWIGEVFFSGSTIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            typing reagents of high specificity and reliability. They can also be used in passive immunisation to prevent haemolytic disease of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 558; DB 2; Length 127;
Prod. No. 1.990-32;
18; Mismatches 27; Indels 1: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The DNA sequence of eleven monoclonal antibodies are represented in 0119145-57. Synthetic genes, for both heavy and light chains may be created by combining selected CDR 1, 2, and 3 regions, which may be selected from different antibody mols. having varied binding specificity. The chimaeric anti-Rhu antibodies can be
                          2. Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding complementary determining regions - of human
Pred. No. 1.68e-32;
15; Mismutches 26, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-rhesus D antibodies, useful in prodn. of monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-human RhD FOG-B MAD (VH chain).
Membelonal antibody, thesus D. blood-typing; CDR;
haemolytic disease of the newborn; HDN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibodies and for passive immunisation
Disclosure, Fig 4; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R12265 standard; Protein; 127 AA. R12265;
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(RL70-) ZENT BLOCD LAP AUTH.
Hughes- Jones N;
WPP: 91-178104/24.
N-PSDP: Q11947.
Best Local Similarity 65.9%;
Natches 83, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 62.8%;
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 AA;
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                                                                                                                                                                                                                                                                                                              119 tvtvss 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 ynpslksrvtisvdasnnqfslklssvtaadtavyycartspqyyd--lltgsfpsywgg 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 YNPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCARSPIKMNQGRMMLDAF-DIWGQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | EVQLLESGPGLVKPSGTLSLTCTVSGGSI-RSSHWWSWVRQPPGKGLEWIGEVFFSGSTI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 qlqlqesgpglvkpsetlsltctvsgdsisrssyswgcirqppgkglewigtiyysgsty 79\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Caps
            20-AUG-1996 (first entry)
Monocolonal antibody DNA heavy chain against 65 kD hCMV antigen.
Monocolonal reaction; primer, amplify; PCR; light chain; MAb;
Polymerase chain reaction; primer, amplify; PCR; light chain; MAb;
65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis.
                                                                                                                                                                                                                                                                                                   Human monoclonal antibody binds to cytomegalovirus 65 kD antigen
                                                                                                                                                                                                                                                                                                                      produced by primer amplification, used in the diagnosis of hCMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 558; DB 16; Length 475, Pred. No. 1.99e-32; Indels 18; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding complementary determining regions · of human anti-rhesus D antibodies, useful in prodn. of monoclonal antibodies and for passive immunisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-AUG-1991 (first entry)
Anti-human RhD FOM-1 MAb (VH chain).
Monoclonal antibody; rhesus D; blood-typing; CDR; haemolytic disease of the newborn; HDN.
                                                                                                                                                                                                                                                                                                                                                     laim 4; Page 16-18; 22pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T 8
R12269 standard; Protein; 128 AA.
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13-NOV-1989; GB-025590.
(BLOO-) CENT BLOOD LAB AUTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.3%;
66.4%;
                                                                                                                                                          /note- "Mature heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 66.4%;
nes 85; Conservative
                                                                                                                                                                                                                                     (NISN) NISSHINBO IND INC.
(TANA/) TANAKA H.
WPI; 96-154852/16.
N-PSDB; T18059.
                                                                                                                        "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98..117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31..35
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                                                                                                                                                                                                                         18-FEB-1994; JP-021628
                                                                                                                                                                                           13-FEB-1996.
20-FEB-1995; 030742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hughes- Jones N;
WPI; 91-178104/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 gtlvtvss 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 GTLVIVSS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; Q11951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
/label- CDR2
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                                                                                                                                                                        J08038178-A.
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                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                           infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                           Protein
                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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The DNA sequence of eleven monoclonal antibodies are represented in 0119145-57. Synthetic genes, for both heavy and light chains may be created by combining selected CDR 1, 2, and 3 regions, which may be selected from different antibody mols. having varied binding specificity. The chimaeric anti-RhD antibodies can be used for diagnosis and therapy, and are capable of providing bloodtyping reagents of high specificity and reliability. They can also be used in passive immunisation to prevent haemolytic disease of the
                                                                                                                                                                                                                                                                                                                                             60 npslksrvtmsvdtskngfslklssvtaadtavyyrarglerpirngllnrlgyymdvwg 119
                                                                                                                                                                                                                                                                                                                                                               61 NPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCARSPIKMNGGRMM--LDAF-DIWG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      claim 9; Page 213; 248pp; Engilsh.

Lymphocyte mRNA was converted to CDNA and subjected to PCR amplification using primers specific for heavy and light chain variable regions. The amplification products were inserted into a dicistronic vector to produce a library of fragments. E.coli XLI Blue cells were transformed with the library, Filamentous phade were produced which expressed the MAD regions on their surface. Panning with gp120 and gp41 resulted in the recovery of immunoreactive clones. The heavy chain VH region sequence R54270 neutralises HIVI
                                                                                                                                                                                                                                                                          1\ {\tt qvqlqqwqaqllkpsetlsltcavyqqsf-sqyywnwirqppqkqlewiqelihsqstny}\ 59
                                                                                                                                                                                                                                                                                              4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-HIV gp41 immunoglobulin heavy chain V region clone DL 41 19. Human immunodeficiency virus; HIV1; glycoprotein gp41; epitope; neutralisation; monoclonal antibody; heavy chain; variable region; framework region; complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gpl20 or gp41 and nucleic acid encoding them, useful for in vivo or in vitro diagnosis and for passive inmuno-therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human monoclonal antibodies neutralising HIV - react with
                                                                                                                                                                                                       Length 128;
                                                                                                                                                                                                                                           22; Mismatches 22; Indels
                                                                                                                                                                                                         Score 556, DB 2, 1
Pred. No. 2.83e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lerner RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R54270 standard; protein: 126 AA.
Disclosure; Fig 8; 32pp; English.
                                                                                                                                                                                                         Match 60.1%;
Local Similarity 62.8%;
les 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-SEP-1992; US-954148.
(SCRI ) SCRIPPS RES INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33..46
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                                                                                                                                                                                                                                                                                                                                                                                                                         120 kgttvtvss 128
                                                                                                                                                                            128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 QCTLVIVSS 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09407922-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= FR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label= FR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barbas CF,
                                                                                                                                                                            Sequence
                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R54270;
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                                                                                                                                                                                                                                                Matches
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Monoclonal antibody, MAD; envelope, glycoprotein, gp120, HIV, AIDS;
CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          represents a naturally occurring polyreactive antibody which binds to many antigens. Ab26 shares greatest sequence similarity with germline VV \ 71-4.
                       04-AUG-1995 (first entry)
Memon Limonoglobuli: variable heavy chain #52.
Primer: PCR. amplify human: immuncylobulin variable, heavy chain, cosmid; placents: Vector: pJB81: E.coll; mammalian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vh 71-4 gene (042697).
Ab26 (042702) was derived from CD5· B cells of a healthy donor and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 64; 109pp; English.
The nucleotide sequence of rearranged F105 Vh (942698) was compare to two monoclonal antibodies (Ab26 · 942702) and 268·D · 942703), which by nucleotide sequence analysis, appear to use a rearranged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA segments encoding menoclonal antibody - which binds to gpl20 and neutralises HIV, for treating AIDS, and for diagnosing and monitoring HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 550; DB 7; Length 116; Pred. No. 8.04e-32; 10; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haseltine WA, Marasco WA, Posner MP, Sodroski JG;
WPI; 93-214174/26
N-PSDB; Q42697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 npslksrvtisvdtskngfslklssvtaadtavyycar 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-DEC-1991; US-804652.
(DAND ) DANA FAPREP CANCEP INST INC.
(NEWE-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epitope; immune deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T 12
R66346 standard; Protein; 116 AA.
                                                                                                                                                                                                                                                                                                                                                   R42689 standard; Protein; 116 AA
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Best Local Similarity 78 6%;
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1993 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= sig_peptide
Protein 20..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'label= mat_protein
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10-DEC-1991; US-8048
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                                                                                                                                                        119 vss 121
                                                                                                                                                                                                                     124 VSS 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     vh 71-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                    P42689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chain;
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ID R6
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Example 3; Fig 18; 366pp; English.

Example 3; Fig 18; 366pp; English.

Example 3; Fig 18; 366pp; English.

The sequences given in W01315-19; represent the heavy chain variable regions (VH) of a series of antibody fragments (FAb's) which are immunoreactive with HIV glycoprotein gp41. This sequence represents chains which bind to chook, DL 41 19. These sequences represent heavy chains which bind to othe light chain clones given in W01320-24. A monochonal antibody containing one of these Pab sequences may have the assay by 50 % at a concentration of less than 700 ng of antibody/m1. The MAD may be used for determining immunocompetence of a human anti-HIV antibody and in the detection of HIV infection.
                                                                                                                                                                                                                                                                                                                    60 lrsrvtmsrdtskngfsvkltsvtaadtalyycarentgrtieeig-nffdiwgggtlvt 118
                                                                                                                                                                                                                                                                                                                                                                                 64 LNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCAPSPIKMNÇGPMMLNAFNIWÇQTTLVI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 llesgpglvkpsetlsltctvsggslssfdw-nwirgpagkglewigriypsgnthynps 59
                                                                                                                                                                                          1 llesgpglvkpsetlsltctvsggslssfdw-nwirqpagkqlewigriypsgnthynps 59
                                                                                                                                                                                                                                                    4 LLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSTIYNPS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 59.8%; Score 553; DB 19; Length 126; Best Local Similarity 66.7%; Pred. No. 4.77e-32; Matches 82; Conservative 14; Mismatches 25; Indels 2; Caps
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                                                                                                                             Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VH of Fab DL 4119, binds to HIV 9941.
Heavy chain; light chain; variable region; VH; monoclonal antibody; MAD; HIV; human immunodeficiency virus; glycoprotein; gpl20; clone; virus infectivity assay; precursor gpl60; immunocompetence; human; anti-HIV antibody; detection; HIV infection.
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                                                                                                                          ći
                                                      Score 553; DB 10; Length 126; Pred No 4 776-72;
                                                                                                                          Indels
                                                                                                                      Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUL-1995; U08743.
18-UL-1994; US-278852.
(SCRI ) SCRIPS RES INST.
Barbas CF, Burton DR, Lerner RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W01315 standard; Protein; 126 AA W01315;
                                                         59.88;
                                                                                        Local Similarity 65.78;
nes 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96-179601/18.
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VH of Fab DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
/label- CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 vss 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 VSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label- CDF1
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Sednence
                                                             Query Match
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1; Gaps

US-08-844-215-6.rag

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DNA fragment comprising human immunoglobulin vh genes - for the production of human immunoglobulin in mammalian hosts production of human immunoglobulin in mammalian hosts production of human immunoglobulin in mammalian hosts.

Bisclosure: Page 107-108: 130pp: Japanese.

Comparison sequences (Re6295-51) are novel human immunoglobulin heavy chain comparison sequences encoded by novel isolated genes. The genes (078919-79002) were sequences encoded by novel isolated genes. The genes are subdivided into 5 families of Vh genes. The Comparison of 800 kb. The DNA fragments were isolated from comparison of 800 kb. The DNA fragments were isolated from the pagested with TagI restriction enzyme. The fragments were separated by digested with TagI restriction enzyme. The fragments were separated by colored with Claif gested cosmid vector pJ881. The fragments comparison and 35-45 kb fractions were collected. The fragments conducts were in vitro packed and infected into E.coli 490A. The products were then subcloned by colony hybridisation. The Vh genes and the DNA fragments encoding them are useful in producing human immunalian hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
useful for treating autoimmune disease or graft-versus-host disease
claim 14. Fig 10B; B1pp; English.

2 Polypeptides (W01821 and W01822) respectively comprise primatised
forms of the light and heavy chains of cynomolgus monkey anti-human
B7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and
heavy variable genes (see also T62512 and T62513) are inserted into
a expression vector (pref. NEOSPLA) which contains human light and
heavy chain constant region genes to allow prodn. of the primatised
antibodies have also been produced (see also W01817-20). The
primatised antibodies inhibit the B7:CD28 pathway, making them
useful immunosuppressants for the treatment of autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 qvqlqesgpglvkpsetlsltctvsggsv-ssyywswirqppgkglewigyiyysgstny ^{78}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSTIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAY-1997 (first entry)
Primatised anti-human B7.1 antigen antibody 16C10 heavy chain.
Monoclonal antibody: Cynomolgus monkey; macaque; 16C10;
primatised antibody: B7 antigen; CD28; immunosuppressive;
autoimmune disease; idiopathic thrombocytopaenia purpura;
systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
type 1 diabetes mellitus; graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brams P, Hanna N, Shestowsky WS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 npslksrvtisvdtsknqfslklssvtaadtavyycar 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 550; DB 12;
Pred. No. 8.04e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W01822 standard; Protein; 476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hetero-hybridoma; transfectoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.5%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric Macaca cynomolgus;
Chimeric Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 78.6%;
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUN-1996; U10053.
07-JUN-1995; US-487550.
(IDEC-) IDEC PHARM CORP.
                                                                  (NISB ) JAPAN TOBACCO INC
24-NOV-1994.
10-MAY-1993; J00603.
10-MAY-1993; WO-J00603.
                                                                                             Matsuda F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97-108638/10.
                                                                                                Honjo T, Matsuda
WPI; 95-006791/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; T62513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9640878-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anderson DR,
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20 qvqlqesgpglvkpsetlsLtctvsgqsvssgsyywswirqppqkglewigyiyysqstn 79
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                                                                                                                                 80 ynpslksgytistdtskngfslklnsmtaadtavyycvrdrlfsvvg-mvynnwfdvwgp 138
                                                                                                                                                       60 YNPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCARSPIKMNOGRMMLDA-FDIWGO 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
59.4%; Score 549; DB 12; Length 118;
Best Local Similarity 77.8%; Pred. No. 9.57e-32;
Matches 77; Conservative 10; Mismatches 11; Indels 1; Gaps
                                                                               20 qvqlqesgpglvkpsetlsltcavsgqsisggygwgwirqppqkqlewiqslysssqnty 79
                                                                                                         1 EVQLLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVROPPGKGLEWIGEVFFS GST1 59
                                                                                                                                                                                                                                                                                          04-Aug-1995 (first entry)
Human immunoglobulin variable heavy chain #54.
Primer: PCR: amplify: human; immunoglobulin; variable; heavy chain; osmid; placenta; vector; pJB81; E.coli; mammalian.
                                                          3; Gaps
                                Length 476;
                                                Pred. No. 8.04e-32;
19; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoglobulin rB6B7 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 ynpsiksrvtisvdtsknqfslklssvtaadtavyycar 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 YNPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYYCAR 98
                                   Score 550; DB 20;
Pred. No. 8.04e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W24536 standard; Protein; 136 AA
                                                                                                                                                                                                                                                        T 14
R66348 standard; Protein; 118 AA.
and graft-versus-host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-OCT-1997 (first entry)
                                    Ouery Match
Best Local Similarity 62.5%;
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        (NISB ) JAPAN TOBACCO INC. Honjo T, Matsuda F;
                                                                                                                                                                                                                                                                                                                                                                                10-MAY-1993; J00603.
10-MAY-1993; WO-J00603.
                                                                                                                                                                                                                                                                                                                                                                                                                                  95-006791/01.
                476 AA;
                                                                                                                                                                                          139 gvlvtvss 146
                                                                                                                                                                                                                    119 GTLVIVSS 126
                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                      24 - NOV - 1994
                Sequence
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Antibody containing immunoglobulin heavy chain mutation - with thyroid function stimulating activity claim 31; Page 14-15; 18pp; Japanese.

W24536 W24539 represent the immunoglobulin heavy and light chain variable regions isolated from peripheral blood lymphocyte strains. These sequences were isolated from the 8687 and 101-2 strains of peripheral blood lymphocytes of a Rasedow's disease patient. These sequences are replaced, deleted or inserted into an antibody, to create the antibodies of the invention. The antibodies of the invention have thyroid function stimulating activity, and act by combining with thyrotropin receptor. The antibody can be used in a method to detect autoantibodies which have thyroid function stimulating activity.
Immunoglobulin; variable region; heavy chain; thyrotropin receptor;
thyroid stimulating activity; light chain; Basedow's disease; antibody;
peripheral blood lymphocyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 nsslksrvtisvdtsknqfslklssvtaadtavyycaree-rggl-rdfaygmdvwgggt 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 qvqlqesgpglvkpsetlsltctvsgdsi-ssyywswirqppgkglewigyihysgstny 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVOLLESGPGLVKPSGTLSLTCTVSGGSIRSSHWWSWVRQPPGKGLEWIGEVFFSGSTIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 69.2%; Pred. No. 1.14e-31;
Matches 83; Conservative 12; Mismatches 22; Indels 3; Gaps
                                                                                      Location/Qualifiers
                                                                                                                                                                                           03-JUN-1997.
22-NOV-1995; 328235.
22-NOV-1995; JF-328235.
(EIKE ) BIKEN KAGAKU KK.
WPI; 97-344899/32.
                                                                                                        Pertide 1..19
/note= "signal peptide"
Protein 20..136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 AA;
                                                                                                                                                                                                                                                                                                    N-PSDB; T79919
                                                                   Homo sapiens.
                                                                                                                                                                     J09140386-A.
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Search completed: Tue Feb 24 07:15:06 1998 Job time: 31 secs.

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Release 2 10 John F Gollins, Riocomputing Poscarch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07:11:04 1999; MasPar time 7.28 Seconds 361 213 Million cell updates/sec

Tabular output not generated

>US-08-844-215-5 Description: Perfect Score:

(1-124) from US08844215.pep 926 1 EVQLLESGGGVVQPGRSLPL. Sedneuce:

IKGRYYLENWGQGTLVTVSS 124

PAM 150 Gap 11 Scoring table:

59021 segs, 21210388 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot34 Database:

lipart1 2 part2 3 part3 4 part4 5 part5 6 part6 7 part7
8:part8 9:part9 10:part10 11:part11

Mean 42.049; Variance 78 185; scale 0.538 Statistics Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	QI	Des	Description	ion		Pred. No.
7	700	75.6	122	רח	HV3C_HUMAN	SI	HEAVY	CHAIN	V · I ! I	2.75e-124
7	619			L)	HV3J_HUMAN	S	HEAVY	CHAIN	V-III	1.15e-119
m	929	73.0	122	Ľ.	HV3H_HCMAN	Ď,	HEAVY	CHAIN	V-III	5.230-119
4	699	72.2	126	'n	HV3K_HUMAN	ij	HEAVY	CHAIN	V-III	1.80e-117
S	636	٠.	119	K)	HV3 I_HITMAN	16	HEAVY	CHAIN	V-III	3.09e-110
9	610	62.9	119	S	HV3L_HUMAN	16	HEAVY	CHAIN	V-III	1 490-104
7	298	٦,	117	S	HV3C_HUMAN	IG	HEAVY	CHAIN	PPECUR	6 16e-102
c c	593	64.0	\sim	S	HV3E_HUMAN	13	HEAVY	CHAIN	V-III	
6	588	63.5	120	'n	HV3U_HUMAN	HG	HEAVY	CHAIN	III-A	9 28p-100
10	584	ς.	~	S	HV3A_HUMAN	ς.	HEAVY	CHAIN	111-A	
11	577	62.3	351	S)	HV16_MOUSE	밁	HEAVY	CHAIN	PPECUP	
12	575	62.1	$\overline{}$	Ŋ	HV3N_HUMAN	1G	HEAVY	CHAIN	1II-A	6.23e-97
13	570	61.6	T-1	r.	HV2T_HITMAN	Ų.	HEAVY	CHAIN	111-A	ď,
14	563	8.09	119	ır.	HV3M_HUMAN	13	HEAVY	CHAIN	V-III	2.51e-94
15	554	59 8	٦	ı,	HV3F_HMAN	Ω	HEAVY	CHAIN	V-III	2 250-92
16	553		$\overline{}$	ı,	HV3D_HUMAN	IG	HEAVY	CHAIN	V-III	
17	S		116	S	HVOS_CARAIT	ŗ.	HEAVY	CHAIN	PPECUP	1.00e-91
18	4	9	\vdash	2	HV3P_HUMAN	IG	HEAVY	CHAIN	V-III	1.21e-90
19	546		142	C)	HV01_PAT	Ď.	HEAVY	CHAIN	PPECTE	1 210-90
20	543		114	r.	HV3B_HUMAN	Ü	HEAVY	CHAIN	V-III	5.41e-90
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	33.22 34.24 35.24 36.25 36

ALIGNMENTS

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1 EVZILESGGGVVQPGPSIRLSCAASGFIFSAASGMHWVPQAPGKGLEWVAGINFGSSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 \hspace{0.1cm} {\tt qvelvesgggvvzpgrs1rlscaasgftfsnyamhwvrqppgkglewvavisybgbbkyy} \hspace{0.1cm} {\tt 60}
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Bost Local Similarity 69.6%, Pred. No. 2.75e-124,
Matches 87, Conservative 26, Mismatches 8, Indels 4, Saps
                                                                                                                                                                                                   LEHMAN D.W., FUTNAM F.W.;
PROC. NATL ACAD SCI U.S.A. 77-3230-3243(10A0).
-!- THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A PATIENT WITH MACROGLORITINEMIA.
                                                                                                         HOMO SAPIENS (HUMAN).
EUKAPYOTA: METAZOA: CHOPNATA: VEPTERPATA: TETPAPODA; MAMMALIA;
EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                PYPROLIDONE CARROXYLIC ACID
                                                                                                                                                                                                                                                                                                              MOD_PES 1 1 PYPPOLIDONE CAFMON NON_TER 122 122 SEQUENCE 122 AA; 13668 MW; 4AF2E3D8 CRC32;
                                                            LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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HV31 HHMAN STANDAPD: PFT: 121 AA. P01771.
21-771-1996 (FEL. 01, CREATED)
21-771-1996 (FEL. 01, LAST SEQUENCE UPDATE)
                PRT;
                                          21-JUJ-1986 (REL. 01, CREATED)
21-JUJ-1986 (REL. 01, LAST SEQUENCE
21-JUJ-1986 (REL. 01, LAST ANNOTATI
IG HEAVY CHAIN V-III REGION (CAM):
                                                                                                                                                                                                                                                                PIR; A02051; M3HUAM.
HSSP; P01607; 2FGW.
IMMUNOGLOBULIN V REGION.
                STANDARD;
                                                                                                                                                                                        MEDLINE: RIG13859
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LT 1
HV3G_HUMAN
P01768;
                                                                                                                                                                           SECUENCE
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1 qvzlvzsgggavzpgrslriscaasgfsfstyamhwvrqapqkglzwlsvisybgbbzyy 60
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                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                      1 qvklvqagggvvqpgrslrlsciasqftfsnygmhwvrqapgkglewvaviwyngsrtyy 60
                                                                                                                                                                                                                                                                   Score 679; DB 5; Length 121;
Pred: No. 1.15e-119;
18; Mismatches 16; Indels 3, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACHWELDRULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-III REGION (HIL).
HOMO SAPIENS (HUMAN).
EUKARYOTA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Indels
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                                                                             PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 63.2%; Pred. No. 5.23e-119;
Matches 79; Conservative 33; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 AA; 13165 MW; D68R085E CRC32;
                                                                                                                                                                        121 121 121 121 121 8E91B7EC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                  P01769;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-III REGION (GA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE: 74175307.
FLORENT G., LEHMAN D., PUTNAM F.W.;
BIOCHEMISTRY 13:2482-2498(1974).
                                                                                                                                                                                                               / Match 73.3%;
Local Similarity 70.2%;
nes 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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HSSP; P01772; 1FGV.
                                                    EUTHERIA; PRIMATES.
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HV3H_HUMAN
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                                                                  EUKAPYOTA; METAZOA; CHOKDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
BUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                   72.2%: Score 669: DB 5; Length 126: 71.4%: Prod. No. 1.80e-117: Atlite 17; Mismatches 17: Indels
                                                                                                                                                                                                     PYRROLIDONE CARBOXYLIC ACID.
                                                                                          SEQUENCE, AND DISULFIDE BONDS.
MEDLINE; 83289131.
SCHMIDT W.E., JUNG H.-D., PALM W., HILSCHMANN N.;
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 364:713-747(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                      13718 MW: 14F3280F (PC32)
                                                                                                                                                 MEDLINE; 81072295.
MARQUART M., DELSENHOFER J., HURFP F., PALM W.;
J. MOL. BIOL. 141:469-391(1980).
J. M. A02055; GHUKL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 AA.
                          21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-III REGION (KOL).
                                                                                                                                       X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
                                                                                                                                                                                               IMMUNOGLOBULIN V REGION; 3D-STRUCTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 71.4%;
90, Conservative
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             STANDARD;
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225
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2IG2; 12-JUL-89.
                                                                HOMO SAPIENS (HUMAN).
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120
126 AA,
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Best Local Similarity
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HV31_HUMAN
P01770;
4 HV3K_HUMAN P01772:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 64.6%;
Local Similarity 81.4%;
Les 79; Conservative
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EMBL; M35415; G553422; -.
PIR; A02047; H3HC26.
HSSP; P01772; IIGM.
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HSSP; P01772; 1FGV.
IMMUNOGLOBULIN V REGION.
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117 AA;
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MEDLINE: 77117574.
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P01764;
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P01766;
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Pred. No. 3.09e-110;
22; Mismatches 12; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Mismatches 15; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOMO SAPIENS (HUMAN).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                      CHOPDATA; VEPTEBRATA, TETRAPODA, MAMMALIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 610; DR 5; Length 119;
Pred No 1 49e-104:
                                                                                                                                                                                            MEDLINE: 77070267.

DREKER L., SCHWARZ J., REICHEL W., HILSCHMANN N.:
HOPPE-SEYLER'S Z PHYSIOL. CHEM 357-1515-1540(1976)

1: THIS CHAIN WAS ISOLATED FROM AN 1531 MYELOMA PROTEIN.
PIR: 542059; 5440NI.
                                                                                                                                                                                                                                                                                           PYRROLIDONE CARROXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYPROLIDONE CAPROXYLIC ACID.
                                                                                                                                      PONSTINGL H., HILSCHMANN N.;
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 357:1571-1604(1976)
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12981 MW, 323A4FE1 CRC32;
                                                                                                                                                                                                                                                                                                                    119 119 119 119 119 AA: 5703CARE GEG32;
21-JUL-1996 (PEL. 01, CPEATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE.UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-III PEGION (NIE)
HOMO SAPERNS (HUMAN).
EUKAPYOTA, METAZOA, CHOPDATA; VEPTEBRATA, TETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (PEL. 01, CPEATED)
21-JUL-1986 (PEL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-III REGION (BUR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUTNAM F.W., LIU Y -S V., LOW T I.K : J. Bloil. CHEM. 254 2865-2874(1979)
PIR: A02056; Altubr.
HSSP: P01772; 1FGV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMUNOCLOBULIN V REGION; GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Best Local Similarity 65.0%;
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 68.5%;
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDAPD;
                                                                                                                                                                                                                                                                              IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96
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119 1
119 AA;
                                                                                     EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUTHERIA; PRIMATES.
                                                                                                                            MEDLINE; 77070269.
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SEQUENCE
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                                                                                                               SEQUENCE
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IMMUNCHEBMISTRY 13:995-999(1976).
-!- THIS CHAIN WAS OFTAINED FPOW ISOLATED FPOW THE SERUM OF A
PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA: VERTEBPATA; TETPAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (PEL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SECOENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
1G HEAVY CHAIN V-III REGION (BRO).
HOMO SAPIENS (HUMAN).
EUKARYOTA: PERAROZA, CHOFFATA, VEFIEBRATA; TETRAPODA, MAMMALIA, EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG BEAVY CHAIN V-II PEGION (VH26)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 81101090.
MATTHYSSENS G., RABBITTS T.H.:
PROC. NATL ACAD. SCI U.S.A. 77:6561-6565(1080).
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Pred. No. 6.16e-102;
12; Mismatches 6;

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      gdsvkgrffisrdnevnilylqms/linedtavyyca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (PEL 01, CPEATED)
21-JUL-1986 (PEL, 01, LAST SEQUENCE UPDATE)
01-OCT-1996 (PEL, 34, LAST ANOTATION UPDATE)
IG HRAVY CHAIN PPECURSOP V-III REGION (VH26).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 evglvesggdlvqpqrslrlscaasgfnfheynmhwlrqgpgkgpewvstitw-nqgsvl 59
                                                                     indels 6; Gaps
                              1 evglvesggglvqpggslrlscaasgftfsyynmnwvrqvtgkglewvsai-gtagdgyy 59
                                                   1 EVOLLESGGGVVQPGRSLRI,SCAASGFTFSAYGMHWVKQAPGKGLEWVAGIWFDGSNQYY 60
                5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
1G HEAVY CHAIN V-III REGION (TRO).
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERIEBRATA; TETRAPONA; MAMMALIA:
                                                                                                                                                                                                                                     HOWO STATEMENS (HUMAN). EUKARYOTA; TETRAPODA; MAMMALIA; EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 120;
                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 588; DB 5; Lk
Fred. No. 9.28e-100:
21; Mismatches 17;
      Best Local Similarity 67.2%; Pred. No. 7.57e-101;
Matches 82; Conservative 20; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                   IMMUNGLOBULIN V REGION.
NON TER 120 120 MW; LUGGESCF CRC32; SEQUENCE 120 AA; 13440 MW;
                                                                                                                                                                                                                                                                                 MEDLINE: 80020921.
STEINER L.A., GARCIA PARDO A., MARGOLIES M.N.:
BIOCHEMISTRY 18:4068-4080(1979).
                                                                                                                                                                                            21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-III REGION (DOB).
                                                                                                                                                                             PRT; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQSENCE (MYELOMA PROTEIN TRO).
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 64.8%,
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                       PIR; A02065; G1HUDB.
HSSP; P01789; 2FGW.
                                                                                                                                                                                                                                                           EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                        80020920
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                                                                                                                                                                                                                                                                                                                                 CRYSTALLIZATION.
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P01762;
                                                                                                                         119 tl 120
                                                                                                                                          118 TL 119
                                                                                                                                                                                  HV3U_HUMAN
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                                                                                                                                                                                                                                                                                 MEDLINE: 81234548.
BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
                                                                                                                                                                                                                          1 EVÖLLESGGGVVQPGRSLRLSCAASGFTFSAYGMHWVROAPGKGLEWVAGIWFFYGSNOYY 60
                                                                                                                                                                                             27; Mismatches 23; Indels 2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IG HEAVY CHAIN V REGION (MOPC 21). D SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; CHORDATA; VENTEBRATA; TETRAPODA: MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5; Length 136;
KRATZIN H., ALTEVUGI F., RUBAN E., KOPIT A., STAROSCIK K.,
HILSCHMANN N.;
                                                                                                                                                                     Length 122;
                                                                                                             PYREGLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 34, LAST ANNOTATION UFGATE)
01-JUL-1996 (REL. 34, LAST ANNOTATION UFGATE)
1G HEAVY CHAIN PRECURSOR V REGION (MORC 21) (FFAGMENT).
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYAD -> DYAH (IN REF. 2
DN -> ND (IN REF. 2).
W -> H (IN REF. 2).
Y -> W (IN REF. 2).
W, 24BFDEBB CRC32:
                                   HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 356:1337 1342(1975).
-!- THE SEQUENCE OF THE C REGION IS ALSO GIVEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.3%; Score 577; DB 5; L
Local Similarity 58 0%; Pred. No. 2.29e-97;
tes 85; Conservative 17. ...
                                                                                                                                                                       Ouery Match
Best Local Similarity 58.1%; Pred. No. 6.89e-99;
Matches 72; Conservative 27; Mismatches 23
                                                                                                                                        122 122 13472 MW; BFC0D3D8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                           136 AA
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NATURE 265:299-304(1977).
EMBL, JO0522: G195055: -.
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMUNOGLOBULIN V REGION; SIGNAL
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1136
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115
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                                                                                                          IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR, A02066; GIMS21.
HSSP; P01607; 1FGV.
                                                                                                                                       122
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136 AA;
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                                                                             PIR; A02045; AlhuTR.
HSSP, F01772; BFAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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CONFLICT
SEQUENCE
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SIGNAL
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IMMINOGLOBULIN V PEGION.
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                                                                      77 adtvkgrftisrdnpkntlflqmtslrsedtamyycar---wqny:-pyyamdywgqgts 131
1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSAYGMHWVPQAPGKGLEWVAGIWFDGSNQYY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VQLLESGGGVVQPGPSLPLSCAASGFTPSAYGMHWVPQAPGKGLEWVAGTW-FD-GSNQY 59
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--- THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACPOSLOBULIN
PIR; A02064; M3HUGL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HILSCHMANN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1996 (REL. 01, CPEATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-III REGION (LAY).
EURARYDENS (HUMAN).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 575, DR 5; Length 119;
Pred No 6 23e-97;
25; Mismatches 13; Indels 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 75046755.
CAPRA J.D., KEHOE J.M.;
PROC. HYLL, ACAS. SCI. U.S.A. 71:4032-4036(1974).
-i- THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA GLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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WATANABE S , BARNIKOL H !! , HORN J., BEPTRAM I , HILS
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 354:1505-1509(1973)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 119
119 AA; 12858 MW; 1CE0116C CRC32;
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21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
11G HEAVY CHAIN V-III REGION (GAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISION TO THE COMPOSITION OF 28-33.
                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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nes 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP, P01772, IIGM.
IMMUNOGLOBULIN V REGION.
NON_TER 119 119
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PIR; A02058; M3HULY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUTHERIA; PRIMATES.
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                                                                                                                                                                                                              132 vtvss 136
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                                                                                                                                                                                                                                                                                 120 VTVSS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 vt 119
                                                                                                                                                                                                                                                                                                                                                                                                                      HV3N_HUMAN
P01775;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 hyadsvngrftisrndskntlyllmnslqarbtalyycarda--gpyvsptffahygggt 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 YYSDSVKGRFTVSRDNSRNTLFLOMNSLRPEDTAVYYCATEVLFGSIKGRYYLENWGOGT 118
                                                                                                                                                                                                                                                         61 vdsvkgrftisrdnaknslylqmnslrvedtalyycarg--wgg--gdy----wqqgtlv 112
                                                                                                                                                                                          1 EVOLLESGGGVVQPGRSLRLSCAASGFTFSAYGMHWVRQAPGKGLEWVAGTWFNGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l evqllesggglvqpggslrlscaasgftfsssamswvrqapgkglewva--wkyengndk 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVÖLLESRAGGVVÖPRARELRESVAASGRIFSAYGMHWVAQAPGKGLEWVAGIW-FD-GSNQ 58
                                                                                                                                                               1 evglvesggdlvqpgrslrlscaasgfbfbblgmtwyrqapgkglewyanikzbgszzby 60
                                                                                                                   8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N -> D (PROBABLY DUE TO DEAMIDATION DURING ISOLATION).
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21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
1G HEAVY CHAIN V-III REGION (BUT).
HOWO SAPINSK (HUMAN).
EUKARYCTA: METAZOA: CHOPDATA; VETTEBRATA; TETRAPODA; MAMMALIA; BUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKAPYOTA, METAZOA, CHOPDATA, VERTEBPATA; TETRAPODA; MAMMALIA.
EUTHERTA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAPPA J.D., KEHOE J.M.;
PROC. NATL. ACAD. SCI. U S A 71-4032-4036(1974).
-:- THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA GLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.8%; Score 563; DB 5; Length 119; 63.4%; Pred. No. 2.51e-94; ative 25, Mismatches 14, Indels
                                                                    Length 116;
                                                                  Score 570; DB 5; Length 116
Pred. No. 7.60e-96;
14; Mismatches 15; Indels
116 116 116 11730 MW; F112826C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 AA; 12953 MW; 2A5697F2 CFC32;
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21-JUL-1986 (PEL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (PEL. 01, LAST ANNOTATION UPDATE)
HOMO SAPIENS (HUMAN).
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                                                                    / Match 61.6%;
Local Similarity 70.2%;
hes 87; Conservative
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nes 78; Conservative
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HSSF, P01772; 1FGV.
IMMUNOSLOBULIN V PEGION.
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MEDLINE; 75046755.
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HV3F_HUMAN
  NON_TER
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RN [1]

RX MEDLINE: 78137069.

RX MEDLINE: 78137069.

RX TORANO A., PUTNAM F.W.:

RA TORANO A., PUTNAM F.W.:

RY TORANO A., PUTNAM F.W.:

INTELOMA PROTEIN IS ALSO GIVEN.

RY MELOMA PROTEIN IS ALSO GIVEN.

RY IMMONGLOBULIN V REGION.

FT NON TER 115 11579 MM; 90803472 CRC32;

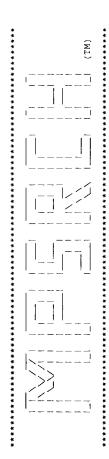
SQUENCE 115 AA: 12379 MM; 90803472 CRC32;

OUETY MATCH

SQUENCE 115 AA: 12379 MM; 90803472 CRC32;

Best Local Similarity 69.0%; Pred. No. 2.25e-92;

Best Local Similarity 69.
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Pelease 2.10 John F. Collins, Riccomputing Pesearch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:11:32 1999; MasFar time 8.34 Seconds 452.970 Million cell updates/sec

Tabular output not generated.

Title: >US-08-844-215-5
Description: (1-124) from US08844215 pop
Perfect Score: 926
Sequence: 1 FVQILFSGGGVVQPSFSLPL.IKGRYYLENWGQGILVIVSS 124

Scoring table: PAM 150
Gap 11
Searched: 95051 seqs, 30469580 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir53

1-annl 2-ann2 3-ann3 4-ann4 5-unann1 6-unann2 7-unann3 8.unann4 9.unann5 10.unann6 11.unann7 12 unann8 13:unann9 14:unann10 15:unann11 16:unann12 17-unann 18:unrev

Statistics: Mean 41.610; Variance 126.095; scale 0.330

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ouery Match Length	DB	ID	Description	Pred. No	
	746	80.6	122	7	531117	g heavy chain -	hum 1.10e-81	
7	720		121	7	S19666	q heavy chain v	3.73e-	~
3	719	77.6	128	7	S48797	chain V	5.1	~
4	713		133	7	A49028	d heavy chain V-	TF 3.326-77	
'n	704	76.0	$^{\circ}$	7	E36005	q heavy chain V	req 5.51e-76	
9	703		132	7	S31603	g heavy chain v	red 7.53e-76	
7	700	75.6	C1	C1	M3HCAM	q heavy chain V-		
α	ÿō9	75 2	۴.	٢	531674	q heavy chain V	Ċ	
6	695	75.1	120	۲.	531112	q heavy chain -	hum 9.12e-75	
10	663		118	7	S31116	heavy chain -	H	
11	069	74.5	C4	7	S36278	q heavy chain V	req 4.33e-74	
13	689	74.4	122	7	869910	O V-D-7 region (u'.	
13	688	74.3	121	^	G36005	q heavy chain V		
14	688	74 3	125	٢	S31598	heavy chain V	red 8.08e-74	_
15	989	74.1	133	1	S31510	heavy chain -	H	~
16	584		-1	۲.	531104	heary chain (Subc 2 818-73	•
17	684	73.9	160	۲-	S05271	heavy chain p	recu 2.81e-73	~
18	683		119	7	S31111	heavy chain -	hum 3.84e-73	~-
19	683	73.8	151	7	A60943	heavy chain pr	ecu 3.84e-73	~
20	629	73.3	121	C1	CIHOHC	heavy chain	II 1.336-72	٠.

119 tvss 122 |||||| ||21 TVSS 124

95. 53.

577 77 76 673 77 658 77	123 7 \$31114 Ig heavy chain - hum 2.49e-72 123 7 \$2693 Ig heavy chain V III 3 39e-72 123 7 \$2693 Ig heavy chain V reg 6.3e-72 123 7 \$2693 Ig heavy chain V reg 6.3e-72 124 7 \$1104 Ig heavy chain V reg 2.19e-71 125 2 \$1107 Ig heavy chain V reg 1.00e-71 126 2 \$1108 Ig heavy chain V reg 1.00e-71 127 7 \$31601 Ig heavy chain V reg 4.09e-71 128 7 \$31601 Ig heavy chain V reg 7.00e-71 129 7 \$31501 Ig heavy chain V reg 7.00e-71 130 7 \$31501 Ig heavy chain V reg 7.64e-70 131 83649 Ig heavy chain V reg 2.64e-70 132 7 \$31107 Ig heavy chain V reg 2.64e-70 133 83649 Ig heavy chain V reg 7.16e-70 126 7 \$31107 Ig heavy chain - human 1.70e-69 127 831107 Ig heavy chain - hum 1.70e-69 128 7 \$31107 Ig heavy chain V reg 2.3ae-69 129 7 \$31107 Ig heavy chain V reg 2.3ae-69 120 7 \$48798 Ig heavy chain V reg 2.3ae-69 121 7 \$31670 Ig heavy chain V reg 4.3ae-69 122 7 \$31107 Ig heavy chain V reg 4.3ae-69 123 7 \$31670 Ig heavy chain V reg 4.3ae-69 124 7 \$31670 Ig heavy chain V reg 4.3ae-69 125 7 \$46790 Ig heavy chain V reg 5.3e-69	ALIGNMENTS 1117 #type complete f heavy chain - human formal_name Homo sapiens #common_name man 16-Nug-1995 #sequence_revision 26-May-1995 #text_change	Timmors, Een, J.M.; Sch. 1 (1942) 22. 11. Intaction of a complement B lymphocyte ts.	translation not show nRNA # 1122 ##label RNA se EMBL:X62967 # 100	80.6%; Score 746; DB 7; Length 122; Conservative 17; Mismatches 7; Indels 2; Caps 2; Conservative 17; Mismatches 7; Indels 2; Caps 2; Gaps 2; Gaps 2; Millillillillillillillillillillillillill
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	$\begin{array}{c} -1 & 0.04 & 0.04 & 0.00$	ULT RY LE ANISM E	SSIONS RENCE authors journal title accession #*statu	##mol ##res ##roro ##not SIFICAT ORDS URE 55-98	hes 9 hes 9 hes 9 1 quq1 1 EVQL

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##residence 1016 ##label MAH
##residence EMBE:246379
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
                                                                                                                   Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Mariet, G. Griffiths, A.D.; Winter, G. J. Mol. Biol. (1991) 222-581-597
By-passing immunization. Human antibodies from V-gene
                                                                                                                                                                                                                                                                                            ##cross-references EMBL:X61646
##cross-references EMBL:X61046
FICATION #superfamily immunoglobulin v region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            548797  #type complete
Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human
#formal_name Homo sapiens #common_name man
#formal_name Homo sapiens #common_name man
13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
        Ig heavy chain'v region (VH3DJH4) - human
#formal_name Homo sapiens #common_name man
22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #domain immunoglobulin homology #label IMM
jth 128 #mclecular-weight 14474 #checksum 9058
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                                                                                                                                                                                                                                                                                                                                                                   #domain immunoglobulin homology #label IMM
th 121 #molecular-weight 13296 #checksum 9195
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Pred. No. 5.10e-78;
13; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       77.8%; Score 720; DB 7; Length 121; 79.0%, Prod. No. 3.73e-78; Ative 14; Mismatches 9; Indels
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      #type complete
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Best Local Similarity 77.3%;
Matches 99; Conservative
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                                                                               16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                               #length 121
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Timmers, B.; Kenter, M.; Thompson, A.; Kraakman, M.E.;
Timmers, J.E.; Alt, F.W.; Schuurman, R.K.
Berman, J.E.; Lississ-2363
Eur. J. Immunool. (1991) 21:2355-2363
Diversity of immunoglobulin heavy chain gene segment
rearrangement in B lymphoblastoid cell lines from X-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schroeder Jr., H.W.; Wang, J.Y. (1990) 87:6146-6150 proc. Natl. Acad. Sci. U.S.A. (1990) 87:6146-6150 proc. Natl. Acad. Sci. U.S.A. (1990) Preferential utilization of conserved immunoalobulin heavy chain variable gene segments during human fetal life.
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iformal_name Homo sapiens #common_name man
21_Dec_1990 #sequence_revision 21.0ec_1990 #tovt_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Mismatches 12; Indels 1; Gaps
61 SDSVKGRETVSPONSRNTLFLOMNSLRPEDTAVYYCATEVLFGSIKGRYY----LENWGO 116
                                                                                                                                                                                 Igheavy chain vill region - human (tradment)
#formal_name Homo sapiens foommon_name man
21.Jan-1994 #sequence_revision 18-Nov-1994 #text_change
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#length 133 #checksum 8516
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77.0%; Score 713; DB 7; Length 133;
Best Local Similarity 77.4%; Pred. No. 3.32e-77;
Matches 96; Conservative 15; Mismatches 12; Indels
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##residues 1-122
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Mechanisms that generate human immunoglobulin diversity, operate from the 8th week of gestation in feral liver. $31603
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Pred. No. 7.53e-76;
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*#cross-references GDB-128528
#map_position 14q32.33-14q32.33
*SSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
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FICATION *Supertamily immunoglobulin V region; immunoglobulin homology
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#authors Lehman, D.W.; Putnam, F.W.
#journal Proc. Natl. Acad. Sci. U.S.A. (1980) 77-3239-3243
#title Amino acid sequence of the variable region of a human mu chain: location of a possible J-H segment.
#cross-references MUID:81013859
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submitted to the EMBL Data Library, June 1992
Mechanisms that generate human immunoglobulin diversity
operate from the 8th week of gestation in feral liver.
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22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
16-Aug-1996
                                                                                                                                                                                                                                                                                                   This mu chain was isolated from the plasma of a patient with
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#length 122 #mclccular-weight 13568 #checksum 7281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heterotetramer; immunoglobulin; pyroglutamic acid
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Fred. No. 6.68e.75,
14; Mismatches 9; Indels
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Ig heavy chain V region - human (fragment)
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M.J.D.; Vossen, J.M.; Schuurman, R.K.B.
Eur. J. Immunol. (1992) 22:247-251
Reskiriched utilization of germ-line V(H)3 genes and short
diverse third complementarity-determining regions (CDR3) in
human fetal B lymphocyte immunoglobulin heavy chain
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Eur. J. Immunol. (1992) 22:247-251
Restricted utilization of germ-line V(H)3 genes and short diverse third complementarity-determining regions (CDR3) in human feal B lymphocyte immunoglobulin heavy chain
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Library, October 1991
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#formal_name Homo sapiens #common_uame man
02-bec-1993 #sequence_revision 26-May-1995 #text_change
4; Gaps
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#formal_name Homo sapiens #common_name man
02-Dec-1993 #sequence_revision 26-May-1995 #text_change
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rth 120 #molecular-weight 12974 #checksum 8808
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##residues 1.120 ##label GRI
##residues 1.120 ##label GRI
##cross-references EMBL:218830
FICATION #superfamily immunoqlobulin V region; immunoqlobulin homoloqy
bS heterotetramer; immunoqlobulin
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Embleton, M.J.; McCafferty, J.; Baier, M.; Holliger, K.P.;
Gorick, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.R.; Winter,
                                                                          *superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBG J. (1993) 12:725-734
Human anti-self antibodies with high specificity from phage
display libraries.
         61 SDSVKGRFTVSRDNSFNTLFLOMNSLRPEDTAVYCATEVLFGSIKGRYYLENWGOGTLV 120
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    qvqlvesgggvvqpgrslrlscaasgftfssygmhwvrqapgkylewvavisydgsukyy 60

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                                                                                                                                                                                                                 74.8%; Score 693; DB 7; Length 118;
79.0%; Pred. No. 1.70e-74;
Attive 15; Mismatches 5; Indels 6; Gaps
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03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
16-Aug-1996
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                                                                                                                                                   #domain immunoglobulin homology #label IMM
#length 118 #molecular-weight 12778 #checksum 4374
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74.5%; Score 690: DB 7: 1
Best Local Similarity 73.2%; Pred. No. 4.34e-74;
Matches 90: Conservative 18; Mismatches 12;
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1-118 ##label KAA
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Matches 98; Conservative
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the sequence of residues 108-122 and the corresponding nucleic acid sequence are not shown superfamily immunoquoluin V region; immunoquoluin homelogy #superfamily immoclobulin V region; immunoquoluin homelogy #length 125 #nolecular weight 13511 #checksum 583
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*journal Proc Natl Acad Sci. U.S.A. (1990) 87:5146-5150

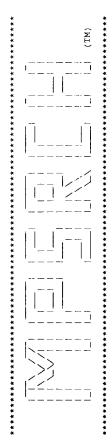
*title Preferential utilization of conserved immunoglobulin heavy chain variable gene segments during human fetal life.

*cross-references MUID:90349571
                                                                                                                                           Sahota, S.; Hamblin, T.; Oscier, D.G.: Stevenson, F.K.
Leukemia (1994) 8:1285-1289
Assessment of the role of clonogenic B lymphocytes in the
pathogenesis of multiple mycloma.
869910
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Ig V-D-J region (KR) - human
#formal_name Homo sapiens #common_name man
14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
09-May-1997
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Ig heavy chain V region (M74) - human
#formal_name Homo sapiens #common_name man
21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change
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**cross-references GB:M34031
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Matches 94; Conservative
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##cross-references EMBL:X69865
FICATION *superfamily immunoglobulin V region, immunoglobulin homology
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                                                                                              Tonnelle, C.
submitted to the EMBL Data Library, June 1992
Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in feral liver
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17, Mismatches 19, Indels
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77 48; Pred. No. 8 086-74;
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##cross-references EMBL:214170
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Search completed: Tue Feb 24 07:12:14 1998 Job time: 42 secs.
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US-08-844-215-5.rpr



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tue Feb 24 07 39 16 1998, MasPar time 3.55 Seconds 177.836 Million cell updates/sec Pun on.

Tabular output not generated.

>US-08-844-215-5 (1-124) from US08844215.pep 926 1 EVQLLESGGGVVQPGRSLRL... Description: Perfect Score:

IKGRYYLENWGQGTLVTVSS 124 Sequence:

PAM 150 Gap 11 Scoring table:

56402 seqs, 5095871 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:backl 2-51 3-52 4-53 5-54 6-55 7-56 8-PCT90 9-PCT91 10-PCT92 11-PCT93 12-PCT94 13-PCT95 14-PCT94

Mean 28.178; Variance 148 297; scale 0.190 Statistics: Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

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Best Local Similarity 78.2%; Pred. No. 1.07e-45;
Matches 97; Conservative 14; Mismatches 8; Indels 5, Gaps
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                                                                                                                                         R INFORMATION: 56P1'CL Variable Heavy chain (V-H)" 119 AA: 13279 MW; 79818 CN;
                                                                                                            LUCATION: 1..119
OTHER INFORMATION: /note= "Human fetal immunoglobulin OTHER INFORMATION: 56Pl'CI Variable "...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA A
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JHN-1995
                                                                                                                                                                                                                                                                                                                                                     125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/375,072 FILING DATE: 25-3AN-1995 PRIOR APPLICATION DATE: US 07/912,292 APPLICATION NUMBER: US 07/912,292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UMBER: US 07/912,292
10-JUL-1992
                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 99, Application US/08478039.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 99, Application US/08478039
  TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEO ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   699 Prince St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READARLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPIOP APPLICATION DATA:
                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5681722
GENERAL INFORMATION:
                                                                amino acid
                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                        STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                      US-08-478-039-99
                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: A
STATE:
                                                                                                                                                                                                                                                                                             116 TVSS 119
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                                                                                                                                                        SEQUENCE
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61 ADSVKGRFIISRDDSKNTLYLQMNSLRAEDTAVYYCAKGQVLYYG-SGSYHWFDPWGQGT 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Michael A.
Braydon C.
SURFACE RESIDUE VENEERING OF KODENT
ANIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 687; DB 7; Length 125;
Pred. No. 4.64e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pensylvania Avenue, N.W.
CITY: Washington
                                                                                                                                                             012712-160
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Hp 9000/700 Workstation
SYSTEM: UNIX
                                                                  US 07/735,064
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                 75 97/856,281
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Anthony R.
                                                                                                                                                                                                                                                                                                                                                                                  CHROMOSOME/SEGMENT: 18/2
NCE 125 AA, 13543 MW, 93321 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 35, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35, Application US/07942245.
                                                                                                                        NAME: Teskin Esq., Robin L. REGISTRATION NUMBER: 35,030
                                                                                                                                                           REFERENCE/DOCKET NUMBER: 01.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                           FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/7
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                             not relevant
                                                                                                                                                                                                                      TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 99:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: PEDERSEN, Jan T. APPLICANT: SEARLE, Stepher APPLICANT: REES, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDAPD;
                                                                                                                                                                                                                                                                        : 125 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                               not relevant
                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                       LECURAL.
TELEPHONE: 703-12
TELEPHONE: 703-836-2021
TYPEAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 73.8%; tes 93; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: not relevan
MOLECULE TYPE: peptide
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
PRIOR APPLICATION DATA: AFFLICATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ROGUSKA, PAPPLICANT: ROGUSKA, PAPPLICANT: GUILD, ITITLE OF INVENTION: STITLE OF INVENTION: AN NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         In house
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SOFTWARE: In hous
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Satent No. 56460...
GENERAL INFORMATION:
APPLICANT: OSEDERG, Lars G.
TITLE OF INVENTION: PPOPURTION OF HIMAN MONOCLONAL
TITLE OF INVENTION: ANIBODIES SPECIFIC FOR HEPAILITS B SUPFACE ANIIS
                                                                                                                                                                                                                                                                                                                                                                                                           Chery Match 73.8%; Score 683; DB 6; Length 141;
Best Local Similarity 77.6%; Pred. No. 9.67e-45;
Matches 97; Conservative 10, Mismatches 14, Indels 4, Gaps
                                                                                                                                                                                                                                                                                                                                                              1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSAYGMHWVPQAPGKGLEWVAGIWFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTE: IRM PG COMPATIBLE
OPERATING: SYSTEM: PG-FW-S-FW-S-FW-S
SOFTWARE: Palentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COFFESPONDENCE ALURESS:
ADPRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CIII: San Francisco
                                                                                                                                               NAME: Smith, William M.
PFOTETRATION NUMBER: 30,223
PFFERENS/COCKET NUMBER: 11823-50-7
TELECOMMINICATION INFORMATION:
      APPLICATION NUMBER: US 07/538,796 FILING DATE: 15-10N-10400 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/192,754 PTIING DATE: 11-MAY-1988
                                                                          UMBER: US 06/925,196
31-OCT-1986
                                                                                                              US 06/904,517
                                                                                                                                                                                                                                                                            MOLECULE TYPE: Protein
SEQUENCE 141 AA; 15613 MW; 114738 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08468671.
                                                                                                                                                                                            TELEPHONE: (415) 326-2400 TELEPAX: (415) 576-0300 INFORMATION FOR SEC ID NO. 2 SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                        TYPF: amino acids TOPPLOGY: 11.
                                                                                                                         05-SEP-1986
                                                                                                                         FILING DATE: 05-SEP-1986 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                             PRIOR APPLICATION DATA - APPLICATION NUMBER: 1 FILING DATE - 31-OCT-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111-3834
COMPUTER READABLE FORM:
                                                                                                PRIOR APPLICATION DATA APPLICATION NUMBER
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        APPLICANT: Ostberg, Lars G.
IIILE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
IIILE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPAIIIIS B SURFACE ANTIG
                                                                                                                                                                                                                                                                                                     61 ADSVKGPFTISRDNSKNTLYLQMNSLRAEDTAVYYGARDRK-DW--GWALFDYWGQSTLV 117
                                                                                                                                                                                                                                                       Match 73.9%; Score 684; DB 7; Length 120; Local Similarity 77.2%; Pred. No. 8.05e-45; es. 95; Conservative 14; Mismatches 11; Indels 3; Gaps
                                                                                                                                                                                                                                           1 QVQLVESGGGVVQPGPSLPLSCAASGFTFSSYAMHWVPQAPGKGLEWVAVISYRGSNKYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Felease #1 0, Version #1 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,372A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COPPESSED ADDRESS: ADDRESSE: Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Lownsens STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                            141 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                            FRT,
                                                                                                                                                          MOLECULE TYPE: peptide
JENCE 120 AA, 13421 MW, 78517 CN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08259372A Patent No. 5565354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/98259372A.
                                                            TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7060
TELEX: 6491103
INFORMATION FOR SEQ ID NO. 35-
SEQUENCE CHARACTERISTICS-
LENGTH: 120 mmino acids
TYPE: amino acid
TOPOLOGY: linear
                            FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                            STANDARE
       CURRENT APPLICATION DAIA: APPLICATION NUMBER: US
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CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5565354
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                           US-08-259-372A-2
                                                                                                                                                                                                                                                                                                                                      118 TVS 120
                                                                                                                                                                                                                                                                                                                                                              121 TVS 123
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                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                             Query Match
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1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSA1SGSGGSTYY 60
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                                                                                                                                                SUPTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DARA: APPLICATION NUMBER: PCT/HS02/1/nr/nr/FITINN NOTE:
EET: Spensley Horn Jubas & Lubitz
EET: 1880 Century Park East - Suite 500
': Los Angeles
E: California
"RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SmithKline Beecham, Corporation APPLICANT: U. S. Government, Secretary of APPLICANT: the Navy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U. S. Government, Secretary of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 43, Application PC/TUS9308435.
                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DUS/MS-DUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ION: 1..125
125 AA; 13464 MW; 94507 CN;
                                                                                                                                                                                                                                             MAME: HOWELLS, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                          TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                               Floppy disk
                                                                                                                                                                                                         29-UCT-1993
                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    125 amino acids
                NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                             FILING DATE:
                                                                                                                                   MEDIUM TYPE:
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                                                                                                       90067
                                           ADDRESSEE:
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APPLICANT:
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                                                                                            COUNTRY:
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                                                          STREET:
                                                                                STATE:
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TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 ADSVKGRFTISRDNSKNTLFLQMHSLRAADTGVYYCAKDQLYFGSQSPGHY----WVQGTL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSPYGMHWVPQAPGKGLEWVAVISYDGSNKWY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | FVOLLESGGGVVQPGRSLRLSCAASGFTFSAYGMHWVRQAPGKGLEWVAGIWFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 9.67e-45:
10; Mismatches 14; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 125 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 683; DB 7; Pred. No. 9.67e-45:
                                                                                                                                                                                                                                                                                                                                                      RESTRAIN WOMEN TO THE STATE OF TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NIMBER: US 06/904.517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                           APPLICATION NUMBER US 07/538,796
FILING DATE: 15-UN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
                                                                                                                      FILING APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FTLING DATE: 27-MAR-1991
                                                                                                UMBER: US 07/871,426
21-APR-1992
                       APPLICATION NUMBER: US/08/468,671
                                                                          US 08/259,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
JENCE 141 AA; 15613 MW; 114738 CN;
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                                 FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 14-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                  : 141 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                 NAME: Smith, William M.
REGISTRATION NUMBER: 30
                                                                                                                                                     FILING DATE: 27-MAR-1
PPIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 15-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 77.6%; es 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.8%;
                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US93-10555-1
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Novel Antibodies for Conterring Passive
Immunity Against Infection by a Pathogen in Man
                            61 ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCTKGQVLYYG-SGSYHWFDPWGGGT 119
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IIILE OF INVENTION: Novel Antibodies for Conferring Passive TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man NUMBER OF SEQUENCE: 61
CORPRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PDTVTGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCASLIYYG-YDG-YAMDYWGQGTLV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVAEISLGGGSYTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVQLLESGGGVVQPGRSLPLSCAASGFTFSAYGMHWVPQAPGKGLEWVAGIWFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 72.8%; Score 674; DB 11; Length 122; Best Local Similarity 75.0%. Pred. No. 5.05e-44; Matches 93; Conservative 14: Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DGS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURPENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US93/08435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SmithKline Reecham, Corporation APPLICANT: U. S. Government, Secretary of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: the Navy
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Army
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSE: Howson and Howson
STREET: Box 457, 321 Norristown Road
CITY: Spring House
                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: SEC P50107 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                               PRIOR APPLICATION DATA-APPLICATION NUMBER: US 07/941,654 FILING DATE: 09-SEP-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application PC/TUS9308435 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
JENCE 122 AA; 13313 MW; 87403 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application PC/TUS9308435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Howson and Howson
                                                                                                                                                                                                                                                                                     NAME: Bak, Mary E. PEGISTRATION NUMBER: 31,215
                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (215) 540-2200
TELEFAX: (215) 540-5200
INFORMATION FOR SEQ ID NO. 43.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                 : 122 amino acids
amino arid
                                                                                                          COMPUTER READABLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                   CLASSIFICATION:
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                                                                                         19477
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PCT-US93-08435-14
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                                                                    STATE:
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APPLICANT: SmithKline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: U. S. Government, Secretary of
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Army
APPLICANT: the Army
IIILE OF INVENTION: Movel Antibodies for Conferring Passive
NUMBER OF SEQUENCES: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SDSVKGPFTVSPONSPNTLFLQMNSLPPEDTAVYYCATEVI.FGSIKGPYYEENW3GGTLV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVULLESGGGLVÖPGGSLRLSCAASGFTFSSYAMSWVPQAPGKGLEWVSEISDGGSYTYY 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                     OPERATING SYSTEM: POT-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBEP: PCT/NS03/08435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 AA.
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 Box 457, 321 Norristown Road
                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: SBC P50107
TELECOMMUNICATION INPOPMATION:
TELEPHONE: (215) 540-9200
TELEPHONE: (215) 540-5818
INPOPMATION FOR SEQ. ID NO: 14:
SEQUENCE CHARACTERISTICS.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
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JENCE 122 AA; 133229 MW; 88138 CN;
                                                                                                                                                                                                                                           NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
                                                                                           COMPUTER: IBM PC compatible
                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                      122 amino acids
                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
STREET: Box 457, 3. CITY: Spring House
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                                                    19477
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                                          COUNTRY:
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US-08-305-583A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SDSVKGRFTVSRDNSRNTLFLQMNSLRPEDTAVYYCATEV1.FGSIKGRYYLENWGQGTIV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSEISDGGSYTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVOLLESGGGVVQPGRSLRLSCAASGFTFSAYGMHWVRQAPGKGLEWVAGIWFDGSNQYY 60
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Michael A.
Braydon C.
SURFACE PESIDUE VENEERING OF PODENT
                                                                                                                                                                                                                                                                                                                                                                                                                  Match 72.4%; Score 670; DB 11, Length 122;
Local Similarity 74.2%; Pred. No. 1.05e-43;
les 92; Conservative 14; Mismatches 16, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas STRBET. 2100 Pensylvania Avenue, N W CITY: Washington
                                                                                 SOFTWARE: Patentin 1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
                                                                                                                                                                                                                            REGISTRATION NUMBER: 31,215
RECISTRATION NUMBER: 3E P50107
REFERENCE/DOCKET NUMBER: SEC P50107
TELECOMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEPAX: (215) 540-5818
INFORMATION FOR STO, 10 no: 12:
SEQUENCE CHARATERISTICS:
LENGTH: 122 amino acids
                                                                                                                                           CLASSIFICATION.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-5EP-1992
ATTORNEY/AGENT INFORMATION:
                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                               LENGTH: 122 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FINCE 122 AA, 13370 MW, 87746 CN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stephen M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 33, Application US/07942245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: PEDERSEN, Jan T. APPLICANT: SEARLE, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RY: United States 20037-3202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: REES, And
APPLICANT: ROGUSKA, MICA
APPLICANT: GUILD, BRE
TITLE OF INVENTION: SURF
TITLE OF INVENTION: ANT
NUMBER OF SEQUENCE: 522
CORRESPONDENCE ADDRESS:
                              COMPUTER READABLE FORM.
                                                                                                                                                                                                                  Bak, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5639641
GENERAL INFORMATION:
                                                                                                                                  FILING DATE:
                19477
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    COUNTRY:
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61 ADSVKGPFTISPNDSKNTLFLQMDSLPPEDTGVYFCARDGGHGFCSSASCFGPDYWGQGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVQLVQSGGGVVQPGRSLRLSCSSSGFIFSSYAMYWVRQAPGKGLEWVA11WDDGSDQHY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LAKE, Philip
APPLICANT: LAKE, Bribara
APPLICANT: OSTREEG, Barbara
APPLICANT: OSTREEG, LAYER
TILLE OF INVENTION: MONOCLONAL ANTIRONY TO HERPES SIMPLEX
TILLE OF INVENTION: VIPUS AND CFIL LINE PRODUCTING THE SAME
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 660; DB 7; Length 125; Pred. No. 6.59e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19; Mismatches 17, Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRAY APPLICATION DATA:
APPLICATION NUMBER: US/08/305.683A
FILING DATE: 13.5EP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 AA.
                                                                                                                          US/07/942,245
09-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                     MEDIUM TYPE: Floppy disk
GOMPHTER: HP 9000/700 Workstation
                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
JENCE 125 AA; 13631 MW; 85784 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application PS/08305683A
Patent No. 5646041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08305683A.
                                                                                                                                                    FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEFIGNE: (202) 293-7060
TELEX: (202) 293-7860
TELEX: 4491103
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTER(STICS:
LENGTH: 125 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HARFELDT, Elisabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COPPESPONDENCE ADDRESS:
ADDRESSEE: Townsend and To
STREET: 379 Lytton Avenue
CTTY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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                                                                OPERATING SYSTEM: UNIX
                                                                                    SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 69.6%;
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                         linear
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80 GESVKGPFIISPDNSKNILYLQMNSLPAEDTAVYYCAPGG-YG--PGHYFYGLDVWGPGT 136
                                                                                                                                                                                                                                                                                                                                        20 QVQLVESGGGVVQPGRSLPLSCAASGPTFSSHVMHWVPQAPGRGLGWLAVTWYPGSNKAY 79
                                                                                                                                                                                                                                                                                         5; Gaps
                                                                                                                                                                                                                        / Match
Local Similarity 71.3%; Score 660; DB 7; Length 142;
Local Similarity 71.8%; Pred. No. 6.59e-43;
les 89; Conservative 17; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Geneticch, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSE: Geneticch, Inc
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUWIRY: USA
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: 5 25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                           NAME: Liebeschuetz, Joe
REGISTRATION NUMRE: 37,505
REBERBLOG-CAPOCKET NUMRE: 11923-005230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2402
INFORMATION FOR SEQ. 100: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
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19930820
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           US 07/759,279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application PC/TUS9307832
                                                                                                                                                                                     MOLECULE TYPE: protein
JENCE 142 AA; 15758 MW, 111669 CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21, Application PC/TUS9307832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 13-SEP-1991
ATTORNEY/AGEN! INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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APPLICATION NUMBER: (
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GENERAL INFORMATION:
APPLICANT: Genent
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                                                                                                                                                                                                    SEQUENCE
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61 ADSVKGPFTISRDNSKNTLYLGMNSLPAEGTAVYYGAPGRVGY-SLSG-LY-DYWGQGTL 117
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                                                                                                                                                                                                                             Indels 4. Gaps
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APPLICANT: Hanna, Nabil
APPLICANT: Razb, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
                                                                                                                                                                                                 Match 71.18, Score 658, DB 11, Length 122, Local Similarity 75.28; Pred. No. 9.51e-43; es 94; Conservative 15, Mismatches 12, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CUPPENT APPLICATION DATA:
APPLICATION UNDER: US/08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
                                                                                                                                                                                                                                                                                                                                                                                                                                123 AA.
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APPLICATION NUMBER: (% (%,379,072
FILING DATE: 25-JAN-1995
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APPLICATION NUMBER: US 07/912,292
                                                                                                                                                                                                                                                                                                                                                                                                                                PPT;
                                                                                                                                                                          122 AA; 13077 MW; 86439 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 94, Application US/08478039
Patent No. 5681722
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 94, Application US/U8478039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
                                                 PEFERENCE/DOCKET NUMBER 70
TELECOMMINICATION INFORMATION:
                                                                                    TELEFAX: 415/952-9881
TELEEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
21P: 22313-1494
COMPUTER PEADABLE FORM:
MEDIUM TYPE: Floppy disk
FILING DATE: 21-AUG-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0-JUL-1992
                                                                                                                                        LENGTH: 122 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                STANDAPD:
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                                      PEGISTPATION NUMBER:
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US-08-478-039-94
                                                                          TELEPHONE:
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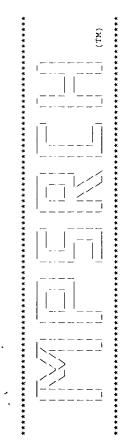
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CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray & ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ADSVKGRFTISRDDSNNTLYMGMNSLRAEDTAVYYCARDRVAVYASVFFIDSFDIWGQGT 120
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                                                                                                                                                                                                                                                                                                                                            Gaps
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APPLICANT: BESPERS, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies -
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC COMPATIBLE
OPERATING SVSTEM: PC-DAS/MS-DAS
SOFTWARE: Patentin Pelease #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                             Score 657; DB 7; Length 123; Pred. No. 1.14e-42;
                                                                                                                                                                                                                                                                                                                                           Mismatches 13; Indels
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                                                                                         TELECOMMUNICATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEBRONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRT;
FILLING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NIMER:
                                           APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 141, Application US/08211202 Patent No. 5565332 GENERAL INFORMATION:
                                                                                                                                                                                                                                                MOLECULE TYPE. peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: RF TS2
JENCE 123 AA; 13515 MW, 82958 CN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 141, Application US/08211202.
                                                                                    NAME: Teskin Esq., Robin L. REGISTRATION NUMBER: 35,030
                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 94: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                        SS: not relevant not relevant
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                                                                                                                                                                                               LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
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Best Local Similarity 72.4%;
Matches 89; Conservative
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60606-6402
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US-08-211:202:141
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STLVERMAN, GREGG J.
VENTION - METHOD FOR STIMULATING PRODUCTION OF
VENTION: VARIABLE PEGION GENE FAMILY BESTRICTED ANTIBODIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLVESGGGVVQPGPSLPLSCAASGFTFSSYAMHWVPQAPGKGLEWVAVISYFKSSNKYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SUSVKGPFTVSPDNSPNTLFLOMNSLPPEDTAVYYCATEVLFGSIKGRYYLENWGQG 117
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Pred No. 1 65e-42;
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1880 Century Park East - Suite 500
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                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFOPMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: anim...
TOPOLOGY: linear
MOLECULE TYPE: protein
TOPOLOGY: 115 AA; 12678 MW, 72426 CN;
TOPOLOGY: ANIMAL AND ANIMAL A
APPLICATION NUMBER, US/08/211,202
FILING DATE: 23.SEP-1992
                                                                                                                                                                                                         FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
                                                                                                                                                                                                                                                                              FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FLING DATE: 24-MAR-1992
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/0088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
                                                                                                                                                                              GB 9120377.8
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 141:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEFERENCE/DOCKET NUMBER 28
TELECOMMUNICATION INFORMATION:
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312-474-6300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          David W. Clough
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: THI
NUMBER OF SEQUENCES: 5:
CORRESPONDENCE ANDRESS:
                                                                                                                                FILING DATE: 23-SEP-3
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
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Best Local Similarity 76 1%:
watches 89; Conscrvative
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California
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                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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PCT-US93-10555-6
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1 EVQLVESGGGVVQPGSSLRLSCAASGFTFSSFAMHWVRQAPGKGLEWVAVMSYSGDNKYY 60
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
CLASSIFICATION:
                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: HOWells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCY/COCKET NUMBER: FD-2630
TELECOMMUNICATION INFORMATION:
TELEPAN: (619) 455-5100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 aming acids
                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Peptide
LOCATION: 1..125
SEQUENCE 125 AA; 13612 MW; 90692 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: Tue Feb 24 07:39:21 1998 Job time : 5 secs.
                                                                                                                                                                                                                                                               STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: RIV
                                                                                                                                                                                                                                                        amino acid
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Matches
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Release 2.1D John F. Collins, Biocomputing Pesearch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07:12:31 1998; MasPar time 7:36 Seconds 234:122 Million cell updates/sec Pun on:

Fabular output not generated

>US-08-844-215-5 (1-124) from US08844±15.pep 926 1 EVQLLESGGGVVQPGPSURL Description: Perfect Score:

.ednence.

IKGRYYLENWGQGTLVIVSS 124

PAM 150 Gap 11 Scoring table:

111726 segs, 13889129 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq30
lpart1 2 part2 3.part3 4 part4 [.part5 6.part5 7.part7
8.part4 4 spart4 10.part10 11.part11 12.part12 13.part13 14:part14 15:part15 16:part16 17.part17 18:part18
19 part10 20.part20 21.part21 22.part12 23.part23

Mean 30.371; Variance 159.298; scale 0.191 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMAPIES

Pesult No.	Score	Query Match I	ength	HQ.	7.0	Description	Pred. No.
Н	206	76.2	192	7	R38161	Sequence of the heavy	7.590-46
7	695	75.1	119	18	R95216	Human foetal immunogi	5.74e-45
3	692	74.7	123	23	W15534	Anti-TGF beta-1 scFv	9.96e-45
4	691	74.6	123	CI.	W13531	Anti-melanoma antibod	1 200-44
Ŋ	069	74.5	111	C3	R12275	Anti-human RhD HAM-R	1.440-44
9	685	74.0	115	4	R22571	Heavy chain VH3.5 fro	3.60c-44
7	684	73.9	120	17	R52064	Heavy chain variable	4.336-44
80	683	73.8	123	53	W15535	Ant: -TGF beta-1 scFv	5 200-44
6	683	73.8	141	5	W01522	Monoclosal antibody P	5.200-44
10	683	73.8	141	د .	W24984	Monoclonal antibody P	5.200-44
11	681	73.5	506	7	F12134	μ_{i}	7.51e-44
12	677	73.1	143	σ	R54047	Sequence of the VH re	1.57e-43
13	674	72.8		σ·	R50315	Humanised heavy chain	2.72e-43
14	673	72.7	125	σ	R54784	SpA-reactive IdM heav	3.26e-43
15	672	72.6	더	6	R50312	Humanised heavy chain	3.92e-43
16	671	72.5		53	W15522	Anti-TGF beta-2 scFv	4 710-43
17	670	72.4	C1	on.	R50311	Humanised heavy chain	5 668-43
18	699	72.2		u)	R28746	Heavy chain variable	6.80e-43
19	668	72.1		23	W13524	Anti-melanoma antibod	8.17e-43
20	564	71.7	117	다 (-)	R56323	Human immunoglobulin	1.70c-42

 1 1 1 1 	.55e-4 .39e-4 .07e-4	07e-4 .28e-4 .54e-4	.20e-4 .20e-4 .20e-4 .67e-4	1.16e-40 1.16e-40 1.39e-40 1.39e-40 1.67e-40 1.67e-40
oti-TGF beta-1 scFv OL heavy chain nti-human RbD REG-A nti-interleukin-1-a	63 antibod 109/112-51 n anti-HBs reactive I	eactive IgM hea nelanoma antibo immunoglobulin chain #3 for a	Sa High	Consensus humanised m Xencerst antibody HA Human TNF binding ant Heavy chain variable Heavy chain #1 for an Anti'HIV Fab rev9(vW3 Human anti-HIV Pab am Anti-melanoma antibod
50000	200 200 406 406	000000000000000000000000000000000000000	01 00 C1 C1	R30773 W06205 R74285 R52065 W13921 R69084 W08733
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00000000000000000000000000000000000000	666 666 656 654	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 7 6 7 6 7	0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	44444444444444444444444444444444444444
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ALIGNMENTS

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freating cancers.

Claim 5: F12:18pp: English.

Claim 5: F12:21 Bpp: English.

Claim 5: F12:21 Bpp: English.

247. PREAUST uses VHIII and a D region which may have resulted from intra D-D recombination and/or gene conversion along with somatic mutation. It is radically different from any germ line D region. It utilises germ line JH3: It is of note that a cysteine at AA posn. Stutilises germ line JH3: It is of note that a cysteine at AA posn.
                                       01-ocr-1993 (first entry)
Sequence of the heavy chain variable region (VH) of human
immunoglobulin G3 (1963) produced by transformed human B-cell line
88BV59, ATCC CRL 10624
                                                                                                                                                                                                                                                                                                                                                                                                                              Crichtón VZ, Haspel MV, Kobrin BJ, WFI: 93-197019/24.
WFI: 93-197019/24.
M-FSDE, 243772.
Iransformed human B-cell line for mencelonal antibody prodn. for cancer diagnosis - prepd from peripheral blood B-cells of cancer patients actively immunised with autologous tumour antigen, for
                                                                                                B-cell; immunoglobulin g; cancer; tumour.
                                                                                                                           Location/Qualifiers
            R38161 standard; Protein; 192 AA.
                                                                                                                                                                   /note= "1st AA is denoted AA#1"
                                                                                                                                                                                                                                                                       112..223
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EP-546634-A.
16-JUN-1993.
29-PE 1992.
13-PEC-1991: US-807300.
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/label= CDR 3
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/label≈ Hinge
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                                                                                                               Homo sapiens.
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/label= CH 1
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                            P38161;
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RESULT
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80 adsvkgrftisrdnskntlylqmnslraedtavyycvkeg-fgsvvvithlafdvwgqgt 138
                                                                                                                                                                                                                                            human variable region heavy chains have a cysteine at this posn. i.e. Kabat posn. 59.
Sequence 192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 13; Figure 11A; 116pp; English.
A novel recombinant DNA molecule which encodes a single chain fusion protein or antibody comprising the for region of both the light and heavy chains of an antibody (Ab) fused together, and an effector molecule, where the fusion protein or Ab has the binding specificity of monoclonal Ab (MAb) B1, B3 or B5, can be used for the production of such fusion proteins or antibodies. The fusion proteins can be used in compositions as an immunoctoxin to inhibit tumour cell growth. The single chain antibody can be used to detect the presence or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             absence of cells bearing a Lewis(Y) carbohydrate antigen in a patient. The antibodies are also useful as multiple targetting moieties, providing at least 2 kinds of biological activity. They can also be used in diagnostic assays and for the imaging of tumours when attached to a radiolabel and for the pathological diagnosis of tumours. Humanised antibodies are less immunogenic than the mouse MAbs B1, B3 and B5, making them more suitable for long term
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single chain fusion proteins and antibodies - useful to diagnose and treat cancer, specifically bind Lewis(Y) related carbohydrate
                                                                                                                                                  20 qvqlvesgggvvqpgrslrlscaasgftfssygmhwvrqapgkgldwvavisydgsneyc 79
                                                                                                                                                                                     1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSAYGMHWVRQAPGKGLEWVAGIWFDGSNQYY 60
                                                                                                               3; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibody; fusion protein; single chain; inhibition; tumour; diagnosis; detection; imaging; immunotoxin; targetting; assay; immunoassay; Lewis(Y) carbohydrate antigen.
                                                                          Score 706; DB 7; Length 192; Pred. No. 7.59e-46;
                                                                                                               12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human foetal immunoglobulin 5681'CL variable heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-OCT-1994; US-33159/.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fitzgerald D, Jun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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R95216 standard; protein; 119 AA.
                                                                                                                 14;
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                                                                            76.2%;
77.0%;
                                                                                               Local Similarity 77.0%;
nes 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Benhar'i, Brinkmann U,
Padlan EA, Pai L, Pasta
WPI; 96-251462/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99..108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-OCT-1994; US-331396.
28-OCT-1994; US-331397.
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Gaps

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Length 119;

Score 695; DB 18; Length 11 Pred. No. 5.74e-45; 14; Mismatches 8; Indels

Query March 75.1%; Best Local Similarity 78.2%; Matches 97; Conservative

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This polypeptide sequence comprises.

Claim 16: Fig la(i): 184pp: English.

This polypeptide sequence comprises the VH domain of human serv antibody iB2 (also known as 7A3), which is specific for cransforming growth fartor (TGP) beta-1. It is encoded by a gene (TG0380) isolated from a peripheral blood lymphocyte library. The antigen-binding domains of human antibodies (see W15522-40) to TGF cantigen-binding domains of human antibodies (see W15522-40) to TGF cantigen-binding domains of human antibodies (see W15522-40) to TGF cantigen-binding domains of human antibodies (see W15522-40) to TGF cantigen-binding domains of human antibodies (see W15522-40) to TGF cantigen-binding domains of historials of human antibodies (see W15522-40) to TGF canting, see the used to counter the adverse offects of tGF beta-1 and/or beta-2 can be used to counter the adverse offects of the canting dibrosis, arterial injury, proliferative telinopathy, retinal detachment, adult respiratory distress syndrome, continosis, solver mayocatian infarction, post-angioplasty inverses, post mayoradial infarction, post-angioplasty inverses, solver mayoradial infarction, cataract, qlaucoma, restencis, scleroderma, vascular disorders, adaract, qlaucoma, cesp. neural scarring and glomerulonephritis, also (not claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 adsekgiftisidaskatlylgmaslraedtavyycaktgeyrggdssg odewqkgitv 119
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Pred. No. 9.96e-45;
15; Mismatches 14; Indels 1; Gaps
                                                                                                                                 61 adsvkgrftisrdnskntlylqmnslraedtavyycarr---sart-yyfdywqqqtlv 115
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l gvelvesggggvygpgrslriscaasgftfssyamhwyrgapgkglewyavisydgsnkyy 60
                                               1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSAYGMHWVRQAPGKGLEWVAGIWFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transforming growth factor beta 1 or 2 - and nucleic acid encoding it, used to neutralise effects of TGF, e.g. for control of fibrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 osteoporosis), or (ii) immune and inflammatory diseases (rheumatoid arthritis, macrophage deficiency diseases or macrophage pathogen infection). Nucleic acids encoding human antibody VH and VL can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used for prodn. of recombinant antiqen binding domains. These are highly specific, have low dissociation constants (prof. less than 5 nM) and low IC50s for neutralisation.
                                                                                                                                                                                                                                                                                                                                                                                                                             27-NOV-1997 (first entry)
Anti-TGF beta-1 scFv antibody 1-B2 VH domain.
Transforming growth factor beta-1; TGF-beta-1; human:
antibody engineering; scFv. phage display: lung fibrosis:
artterial injury; proliferative retinopathy: retinal detachment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            scleroderma; vascular didease; cataract; glaucoma; scarring; glomerulonephritis; osteoporosis; immune disease; inflammation; rheumatoid arthritis; macrophage deficiency disease; macrophage pathogen infection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adult respiratory distress syndrome; liver cirrhosis, post myocardial infarction; post-angioplasty restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agent contg. antigen-binding domain of human antibody to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jackson RH, Johnson KS, Pope AR:
n JE, Vaughan TJ, Williams AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                           W15534 standard; Protein; 123 AA.
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06-OCT-1995; GB-020486.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A process for isolating and synthesising human monoclonal anti-tumour antibodies has been produced. The process involves: (a) constructing at least one fitalion phage library from the peripheral blood hypphocytes (PBLS) of a cancer patient; (b) screening for anti-tumour antibodies in the phage library in a binding assay with cultured tumour cells of the same type as the patient's tumour; (c) removing extraneous antibodies by absorption against normal human cells; (d) cloning the phage salected in step (b) and (c); (e) assaying the specificity of the cloned phage by incubating the phage with at least two types of cultured normal cells; and (f) further testing the specificity of cloned phage that colline of cultured normal cells in further binding assays to either cell line of cultured normal cells in further binding assays of cultured unmour cells derived from more than one other tumour that is not the patient's tumour. The present sequence represents a human heavy chain antibodie, from an screw antibodies produced can be used for a method as described above The antibodies produced can be used for a method as described above The antibodies produced can be used for antigens for studying tumourigenesis or for use as anti-cancer vaccines. The human antibodies have low immunogenicity in humans compared to murine monoclonal antibodies (MABs). Since the antibodies are isolated from common cell line can be improved by genetic manipulations.
61 adsvkgrftisrdnskkntlylqmnslraedtavyycargfpygg-nsdygmdvwdhgtg 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SDSVKGRFTVSRDNSR-NTLFLQMNSLRPEDTAVYYCATEVLFGSIKGRYYLENWGQGTL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 691, DB 23, Length 123,
Prod. No. 1.206-44;
17; Mismatches 12, Indels 2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 gvglvesgggvvqpgrslrlscaasgftfssyamhwvrqapgkglewmarisydgsnkyy 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLLESGGGVVQPGPSLPLSCAASGFTFSAYGMHWVPQAPGKGLEWVAGIWFDGSNQYY 60
                                                                                                                                                                                                                                                   Wi351;
28-CCT-1997 (first entry)
Anti-melanoma antibody heavy chain clone V575.
Human: monoclonal antitumcur antibody; periphoral blood lymphocyte,
rancer; tumourigenesis; anticancer vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prodn. of human monoclonal anti-tumour antibodies - by screening a fusion phage library produced using peripheral blood lymphosytes
                                                                                                                                                                                                                                     W13531 standard; protein; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 19; Page 68; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 75 0%;
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100..113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JAN-1997.
28-JUN-1996; IB1032.
30-JUN-1995; US-497647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50..66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from a cancer patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYYA ) UNIV YALE.
Cai X, Garen A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 AA;
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                                                                             120 trss 123
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                                                                                                                                  121 TVSS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label- CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label- CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
/label- CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09702479-A2
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DNA encoding complementary determining regions - of human anti-rhesus D antibodies, useful in prodn. of monoclonal anti-rhesus D antibodies, useful in prodn. of monoclonal antibodies and for passive indumination Disclosure, Fig 14, 32pp. English.

The DNA sequence of eleven monoclonal antibodies are represented in 0.19145-57. Synthetic genes, for both heavy and light chains may be created by combining selected CDP 1, 2, and 3 regions, which may be selected from different antibody mols. Having varied binding specificity. The chimaeric anti-Rhb antibodies can be used in dargnesis and therapy, and are capable of providing blood-typing reagents of high specificity and reliability. They can also be used in passive immunisation to prevent haemolytic disease of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ggvvqpgrslrlscaasgftfssygmhwvrqapgkglewvaviwydgsnkyyadsvkqrf 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 74.5%; Score 690; DB 2; Length 111;
Best Local Similarity 79.5%; Pred. No. 1.44e-44;
Matches 89; Conservative 13; Mismatches 7; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 GGVVQPGPPSLPLSCAASGPTFSAYGMHWVPQAPGKGLEWVAGIWFDGSNQYYSDSVKGPF 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ed, bacteriophage, gene III, filamentous; plagemid, capsid, coat, plus; 93p, binding, adsorption; gene VIII, diverse repertoire, specific binding pairs, replicable genetic display package, human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MEDI-) MED RES COUNCIL.
McCafferty J. Pupe AP. Johnson KS. Howgenboom HRJ. Griffiths AD.
Jackson RH. Holliger KP. Marks JD. Clackson TP. Chiswell DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 TVSRENSRNILELUMNSLRPELIAVYYCAIEV-LFGSIKGRYY-LENWGUGI 118
                                                                                      15-A0G-1991 (first entry)
Anti-human RhD HAMFA MAP (VF chain)
MOCOCIONAL antibody; thesus D; blood-typing; CPR;
haemolytic disease of the newborn; HDN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heavy chain VH3.5 from BSA binding scFv fragment.
                                                                                                                                                                                                                                                   Location/Qualifiers
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R22571 standard; Protein; 115 AA.
JT 5
R12275 standard; Protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BLOO-) CENT BLOOD LAB AUTH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAY-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   901 16
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12-NOV-1990; GB-024503.
06-MAR-1991; GB-004744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-MAY-1991; GB-010549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-NOV-1989; GR-025590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUL-1991; G01134.
10-JUL-1990; GB-015198.
                                                                                                                                                                                                                                                                                                                                          42..58
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13-NOV-1990; E01964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 91-178104/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hughes - Jones N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; 011957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
W09201047-A.
                                                                                                                                                                                                                                                                             Region
/label= CDR1
                                                                                                                                                                                                                                                                                                                                                                      CERD
                                                                                                                                                                                                                                                                                                                                                                                                                                /label= CDR3
WO9107492-A.
                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                      /label
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per was used too prepare a human scrot library from RNA from white per was used too prepare a human scrot library from IgG and blood cells from an unimumulsed donor. Heavy chains from IgG and blood cells from an unimumulsed donor. Heavy chains from IgG and IgG and antibodies were amplified separately. Four separate libraries were generated (IgG**, IgG-lambda, IgW** and IgW*-lambda). The curie contains were then subjected to affinity selection for binding to phox:BSA by selection on tubes followed by analysis by ELISA. Of these were designated BSA binders. Thirteen of fourteen clones sequenced had the same sequence, the VH derived from a human VH3 sequenced had the same sequence, the VH derived from a human VH family qene (RA2572). The other was derived from a human VH4 family qene and a human VK1 family gene. One clone bound only to phox:BSA and a human VK1 family gene (RA2574) and VL from a human VH4 family qene (RA2574). This sequence revealed a VH derived from a human VK1 family gene (RA2576) and VL from a human V lambda 1 family gene (RA2570). The other was derived from a human VH4 family gene (RA2570). The other was lambda from a human VH4 family gene (RA2570) and VL from a human V lambda I family gene (RA2570).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 qvqlvqsgggvvqpgrslrlscaasgftfssygmhwvrqapgkglewvavisydgsnkyy 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSAYGMHWVRQAPGKGLEWVAGIWFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 685; DB 4; Length 115;
Pred. No. 3.60e-44;
14; Mismatches 9; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 adsvkgrftisrdnskntlylgmnslraedtavyycaktg-yssgwg-yf-dywgggt 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Method of resurfacing of rodent antibodies to produce humanised antibody forms - for producing non-human antibodies with improved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-007-1996 (first entry)
Heavy chain variable region of human G36005 antibody.
antibody, humanised, murine; human; heavy chain: light; variable; framework region; complementarity determining region; reshaping; modelling; surface residue; modify.
                             producing members of specific binding pairs - by expression in recombinant host cells with a secreting replicable genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pedersen JT, Rees AP, Roguska MA, Searle SMJ:
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                                                                                         Table 11; Page 152; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T
R52064 standard; Protein; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 74.0%;
Best Local Similarity 78.0%;
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= framework_region_l
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Winter GP, Bonnert TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPEDEZ) PEDERSEN J T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-SEP-1993; 307051.
09-SEP-1992; US:9422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94-120230/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                             115 AA;
                                                                       display package.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "CDR 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "CDR 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "CDR 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "FR 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "FR 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-APR-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guild BC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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therapeutic efficiency by presenting human surface on V-region

Example 1; Fig 4B; 230pp; English.

Modification of a rodent antibody (Ab) or fragment by resurfacing in

order to produce a humanised rodent Ab can be determined by calculating

context to produce a humanised rodent Ab can be determined by calculating

context to produce a humanised rodent Ab can be determined by calculating

context to produce a humanised rodent Ab can be determined by calculating

context to produce a humanised rodent Ab can be determined antibody surfaces. In order to test

context to produce a humanised rodent Ab can be determined by calculating approach

using most similar chain; and (3) resurfacing approach using human

context to a sequence which may a similar surface residues. The Ab used was the mutine

anti-N901 Ab (see R52064). Experiment 2 was carried out using the present

context to prepd. by congressing with anti-N901 Ab. N901/G36055 (MS2065) was

prepd. by congressing sequence numbering starts at 118 in the

specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agent contg. antigen-binding domain of human antibody to transforming growth factor beta 1 or 2 - and nucleic acid encoding transforming growth factor beta 1 or 2 - and nucleic acid encoding transforming growth factor beta 1 or 2 - and nucleic acid encoding transforming disease.

Tit used to neutralise effects of TGP, e.g. for control of fibrosis, contain 16; Fig la(i); 184pp; English.

Claim 16; Fig la(i); 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVÜLLESGĞĞVVÖPGRSERLSCAASGFTFSAYSMHWVPQAPGRCI.FWVACIWFDCSNOYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 4.33e-44;
14; Mismatches 11; Indels 3: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-NOV-1997 (first entry)
Anti-TGF beta-1 scFv antibody 31G9 VH domain.
Transforming growth factor beta-1; TGF-beta-1; human;
antibody engineering; scFv, phage display; lung fibrosis;
artibody engineering; scFv retinopathy; retinal detachment;
arterial injury; proliferative retinopathy; retinal detachment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      scleroderma; vascular didease; cataract; qlaucoma; scarring; qlomerulonephritis; osteoporosis; immune disease; inflammation; rheumatoid arthritis; macrophage deficiency disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adult respiratory distress syndrome, liver cirrhosis; post myocardial infarction; post-angloplasty restenosis;
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BACOD L, Green JA, Jackson KH, Johnson KS, Pope AR;
Thompset PR, Thompson JE, Vaudhan TJ, Williams AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.9%; Score 684; DB 17; 77.2%; Pred. No. 4.33e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               macrophage pathogen infection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T 8
W15535 standard; Protein; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thompson JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 77.2%;
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07.OCT-1996; 020920.
19-JAN-1996; GB-001081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-OCT-1995; GB-020485.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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61 adsvkgrftisrdnskntlylqmnslraedtavyycartgeysgydtsg-velwgqgttv 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 gvglvgsgggvvgpgrslrlscaasgftfssygmhwvrqapgkglewnavisydgsikyy 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSAYGMHWVRQAPGKGLEWVAGIWFDGSNQYY 60
               Agoular discretes, catract, glaucoma, or esp neural scarring and glomerulonephilis, also (for claimed) ustoupriesis), or (ii) immune and inflammatory diseases (e.g. rheumatory arthritis, macrophage deficiency diseases or macrophage pathogen inferiou) Nucleic acids encoling human antibody VH and VL can be used for prode of recombinant antigen-binding domains. These are highly specific, have low dissociation constants (pref. less than 5 nM)
                                                                                                                                                                                                                                                                                                                                                                             Indels 1, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03.4MR-1997 (first entry)
Monoclonal antibody PE1-1 heavy chain variable region.
Monoclonal antibody; diagnosis; treatment; infection; hepatitis B;
xenogeneic hybridoma, SFAZ 4; FE1-1, CML-1, CML-1, M3-4, L03-2,
IgGl class, heavy chain; light chain; variable region.
myocardial infarction, post-angioplasty restenosis, scleroderma,
                                                                                                                                                                                                                                                                                                                  Score 683, DB 23; Length 123;
Pred. No. 5.20e-44;
14; Mismatches 15, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label- complementarity_determining_region_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                            and low IC50s for neutralisation. Sequence 123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W01522 standard; Protein; 141 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "start of FR3 region"
Region 118.129
                                                                                                                                                                                                                                                                                                                     Match 73.8%;
Local Similarity 75.8%;
les 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- V_H(III)_region
Region 20..49
/label- framework_region_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label = leader_sequence
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27-MAR-1991; US-676036.
21-AFR-1992; US-871426.
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31-CCT-1986; US-925196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54..69
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/label= CDR2
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                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                             Matches
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08-DEC-1997 (first entry)
Monoclonal antibody Bell 1 Wh region.
Heavy chain: light chain; variable region, human, monoclonal antibody:
Immunisation; hepatitis B virus; HBV, vaccine; mouse; fusion, xenogeneic;
peripheral blood hymphocyte; surface antigen; cell culture; ion exchange;
chromatography; size separation; prime; PCR; polymerase chain reaction;
applification, hybridema, infection, immunosuppression; hepatitis;
                                                                                                               from a
            The state of the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 adsvkgrftisrdnskntlflqmhslraadtgvyycakdqlyfgsqspghy---wvqgtl 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SDSVKGRFTVSRDNSRNTLFLQMNSLRPEDTAVYYCATFVL, FGSTKGRYYLENWGQGTL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 qrqlvosgggvvqpgrslrlscaasgftfsrygmhwrrqapgkglowravisydgsnkwy 79
                                                                                                                                                                                                                                                                                                                                          Score 683; DB 19; Length 141;
Prod No. 5 20e-44;
10; Mismatches 14; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVOLLESGGGVVQPGPSLPLSCAASGFTFSAYGMHWVPQAPGKGLEWVAGIWFDGSNQYY 60
Human monoclonal antibodies specific for hepatitis B surface antiden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treatment of hepatitis R - with human monoclonal antibody Example 8, Column 15-18, 25pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entarity determining region 1"
69..85
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                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 77 6%,
Matches 97, Conservative
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"mature protein"
20..117
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15-JUN-1990; US-538796.
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14-JUN-1994; US-259372.
06-JUN-1995; US-468671.
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Domain 50..54
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31-OCT-1986; US-925196
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N-PSDB; T85838.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "complemen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     liver transplant.
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                                                                                                                                                                                                                                                                                               Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
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from the human monoclonal antibody (MAb) PEI-1. The MAb was generated from the human monoclonal antibody (MAb) PEI-1. The MAb was generated by immunising humans with a hepatitis B virus (HBV) vaccine, isolating by immunishing humans with a hepatitis B virus (HBV) vaccine, isolating by propered cell line Spa2-4. 5 cell lines were isolated PEI-1, ZMI-1, Xml-2, MD3-4 and LO3-3. The cell lines were then tested for production of a nati-hepatitis B virus surface antigen antibody by ELISA. The MAbs care then purified from large scale cell culture by protein A care then purified from large scale cell culture by Protein A care then burnatography, size separation on Sephacryl S300 gel and ion exchange chromatography on Q-sepharose. The heavy and light chains of the MAbs canerated and used to amplify cDNA synthesised from RNA purified from generated and used to amplify cDNA synthesised from RNA purified from call horidom cell line. The sequences of the heavy and light chains of (nucleic acid and amino acid) from MAbs PEI-1, ZMI-1, ZMI-2 and MD3-4 are conclusing a mimmunosuppressed patients or peu used to treat HBV increasing the conclusion of the heavy in the chains of the heavy in the chains of the heavy in manuscuppressed patients or peutients with chronic active conclusion of the conclusion of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SDSVKGRFTVSPDNSRNTLFLQMNSLRPEDTAVYYCATEVL-FGSIKGRYYLENWGUGIL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 qvqlvesgggvvqpgrslrlscaasgftfsrygmhwvrqapgkglewvavisydgsnkwy 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSAYGMHWVRQAPGKGLEWVAGIWFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is derived from the nucleotide sequence encoding the heavy chain variable region. The "x" residues represent nonsense codons. The coding sequence has been translated in all 3 reading frames (see also R12132 and R12133).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligomeric immunoglobulin(s) with high avidity for antigen(s) -formed by duplicating esp. variable region of light chain of 19G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin G; heavy chain; variable region; duplication,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 683; DB 23; Length 141;
Pred. No. 5.20e-44;
10; Mismatches 14; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1991 (first entry)
OPF 3 of 4B9 human MAb heavy chain variable region clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       hepatitis, especially liver transplant patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "last 3 residues of leader and variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region; the rest of leader is translated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 passive immunity; group B streptococci.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R12134 standard; Protein; 506 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BRIM ) BRISTOL-MYERS SQUIB.
Shuford WW, Harris LJ, Raff HV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 76 68:
es: 95; Consorred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.8%;
Local Similarity 77.6%;
nes 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244..369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAY-1991.
06-NOV-1990; U06426.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R12134;
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Gaps

Score 681; DB 2; Length 506; Pred. No. 7.51e-44; 14; Mismatches 13; Indels

Query Match

Matches:

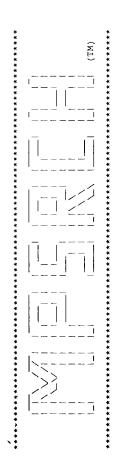
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for diagnosis and treatment differentials by Functional antibodies active addition in the monoclonal antibodies active addition in the monoclonal antibodies and treatment of Hepatitis B virus Example: Page 35: 53pp; English.

Chuman volunteers were immunised with hepatitis B vaccine. MD3-4, ZM1-1 and PE1-1 hybridoma cell lines were derived from 1 ymphocytes of individuals immunised with Heptavax (Merck 6 Co).

Chribodies PE1-1, ZM1-1, MZ1-2 and MD3-4 belong to the 1963 class.

The cell lines producing PE1-1, ZM1-1 and ZM1-2 were deposited as The cell lines producing PE1-1, ZM1-1 and ZM1-2 were deposited as Troches as typical (mouse x human) x human hybridomas and produce their espective Abs in concs. ranging up to 25 mq/1 in standard chains of Abs PE1-1, ZM1-1 and MD3-4 were isolated and chains of Abs PE1-1, ZM1-1 and MD3-4 were isolated and chains of Abs PE1-1, ZM1-2 and MD3-4 were isolated and chains of Abs PE1-1, ZM1-2 and MD3-4 were isolated and cannot be concerned and class and objected from 10(7) hybridoma cells of each cell line. Ss DNA was synthesised using AMV-reverse and objected amplified DNA was size as primer. PCRs were performed and amplified DNA was size as primer. PCRs were performed and amplified DNA was size as primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 gvglvesgggyvgpgrslrlscaasaftfsrygmhwvrgapykglewvavisydgsnkwy 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : THE HITTH HITTHH HIT
247 qvqlvesgggvvqpgislrlscaasgftfrsygmhwvrqapgkglewvavissdqsvdyy 306
                                                                                                                          307 adsvkgrftisrdnsrdmlyvgmnsiraedtavyydakekosggr scysfdywqqqtlv 364
                                                                                                                                                        Gaps
                                                             1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSAYGMHWVPQAPGKGLFWVAGIWFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of the VH region of monoclonal antibody PEI-1 against hepatitis B virus surgace antigen. Hepatitis B virus; surface antigen; monoclonal antibody; thorapy; HBSAG; diagnosis; HBV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monoclonal antibodies active against Hepatitis B surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing was by the dideoxy chain termination method (Sanger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9; Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from each positive clone after superinfection with M13K07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 677; DB 9; ; Pred. No. 1.57e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            R54047 standard; Protein; 143 AA.
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76.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-NOV-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118..129
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Les 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-NOV-1992; U09749.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SANO ) SANDŪZ LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; Q64050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= leader
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= CDR 2
                                                                                                                                                                                                                                                                            365 tvss 368
                                                                                                                                                                                                                                                                                                                                     121 TVSS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JH 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R54047;
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Page 1



Pelease 2 10 John F Collins, Biocomputing Research Unit Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07:09:05 1998; MasPar time 5.26 Seconds 504.498 Million cell updates/sec Tabular output not generated. Run on:

>US-08-844-215-4

1 EVQLLESGGGVVQPGRSLPL. IKGRYYLENWQQGTLVIVSS 125 (1-125) from US08844215.pep 921 Description: Perfect Score: Sequence.

PAM 150 Gap 11 Scoring table:

59021 seqs, 21210399 residues Searched.

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot34 Database:

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11

Mean 42 149; Variance 77.571; scale 0.543

Statistics.

Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Score Match Length DB ID Description Prod 637 73.7 122 5 HV34_HUMAN IS HEAVY CHAIN VIII 7.456-659 73.7 122 5 HV34_HUMAN IS HEAVY CHAIN VIII 7.456-659 1 125 5 HV34_HUMAN IS HEAVY CHAIN VIII 7.456-659 1 125 5 HV34_HUMAN IS HEAVY CHAIN VIII 7.456-62.8 120 5 HV34_HUMAN IS HEAVY CHAIN VIII 1.516-578 62.8 120 5 HV34_HUMAN IS HEAVY CHAIN VIII 1.516-578 62.8 120 5 HV34_HUMAN IS HEAVY CHAIN VIII 1.516-578 62.8 120 5 HV34_HUMAN IS HEAVY CHAIN VIII 1.516-578 60.8 119 5 HV34_HUMAN IS HEAVY CHAIN VIII 1.516-550 60.8 116 5 HV37_HUMAN IS HEAVY CHAIN VIII 1.516-550 60.8 119 5 HV37_HUMAN IS HEAVY CHAIN VIII 1.516-550 60.8 119 5 HV37_HUMAN IS HEAVY CHAIN VIII 1.516-550 60.8 119 5 HV37_HUMAN IS HEAVY CHAIN VIII 1.516-550 60.8 119 5 HV37_HUMAN IS HEAVY CHAIN VIII 6.486-550 60.8 115 5 HV37_HUMAN IS HEAVY CHAIN VIII 6.486-550 60.8 114 5 HV37_HUMAN IS HEAVY CHAIN VIII 6.486-550 60.8 115 5 HV37_HUMAN IS HEAVY CHAIN VIII 6.486-550 60.8 115 5 HV37_HUMAN IS HEAVY CHAIN VIII 6.486-550 60.8 115 5 HV37_HUMAN IS HEAVY CHAIN VIII 6.486-550 60.8 115 5 HV37_HUMAN IS HEAVY CHAIN VIII 6.486-550 60.8 115 5 HV37_HUMAN IS HEAVY CHAIN VIII 6.486-550 60.8 115 5 HV37_HUMAN IS HEAVY CHAIN VIII 6.486-60.8 1	PPS111		ال ال								
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7 534 58.0 114 5 HV3B_HUMAN IG HEAVY CRAIN V-III 6.48 534 58.0 115 5 HV3B_HUMAN IG REAVY CRAIN V-III 6.48 526 51.0 115 5 HV3B_HUMAN IG REAVY CHAIN PPROTIF 7 6.0 524 56.9 142 5 HV5P_MPROTIF IG REAVY CHAIN PSRCTIF 9 92 52 55.9 17 5 HV5P_MPTSE IG REAVY CHAIN PSRCTIF 9 92 52 55.9 17 5 HV5P_MPTSE IG REAVY CHAIN PSRCTIF 9 92 92 92 92 92 92 92 92 92 92 92 92 9	16	536	58.2		Ŋ	HV02_CANFA	IG	HEAVY	CHAIN	V REGI	.37
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9 526 57 1 115 5 HVOS_CARAU IG BEAVY CHAIN PRECUP 3 506- 0 524 56.9 142 5 HVOS_MTSE IG BEAVY CHAIN PRECUP 9 926- 1 521 56.5 97 5 HVOS_MTSE IG BEAVY CHAIN V RECU 4 950- 2 515 55.9 117 5 HVOS_MOUSE IG BEAVY CHAIN V PRECUP 8 950-	18	534	58.0		Ŋ	HV3D_HUMAN	ΡI	HEAVY	CHAIN	V-III	.48e-8
0 524 56.9 142 5 4001 PAT TO HEAVY CHAIN PRECIPE 9 826-1 1 521 56.6 97 5 HEVŠELMINES EGHEAVY CHAIN V PRECI 4 426-2 2 515 55.9 117 5 HVSF. MOTER TO HEAVY CHAIN PRECIPE 8 956-3	19	526		116	ľ	HVOS CAPAU	5	HEAVY	CHAIN	PRECTE	Ψ,
1 521 56.5 97 5 HV55_MMUSE IG HEAVY CHAIN V REGI 4 426- 2 515 55.9 117 5 HV55_MMUSE IG HRAVY CHAIN PREGUP A 956-	20	524	55.9	142	u.	- 1	5	HEAVY	NIARC		ن ت
2 515 55.9 117 5 HV55_MOUSE IG HEAVY CHAIN PRECUP R 950-	21	521	56.6	40	r -	HV55_MOTSE	5	HEAVY	CHAIN		4 420-86
	22	515	55.9	117	u'	HVS. MOTISE	Ç.	HEAVY	CHAIN	Ċř.	950

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HV31_HUMAN
P01770;
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                                                                                                                                                                                         1 EVQLLESGGGVVQPGRSLRLSCAASGFTFKTYGMHWVRQAPGKGLEWVAGISFDGSNQYY 60
                                                                                                                                                                          3; Gaps
                                                               MEDLINE; 74175307.
FLORENT G., LEHMAN D., PUTNAM F.W.;
BIOCHEMISTRY 13:2482-2498(1974)
-!- THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLORULIN.
BIR; A02052; M3HUGA.
HSSP; P01772; 1FGV.
                                                                                                                                                                                                                                                                                                                                                                  HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-III REGION (GA).
HOMO SAPIENS (HUMAN).
EUKARYOTA, METAZOA; CHOKDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                       Score 679; DB 5, Length 122;
Pred. No. 7.46e·121;
30; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYRROLIDONE CARBOXYI,IC ACID.
                                                                                                                         PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE: (83289131.
SCHMIDT W.E., JUNG H.-D., PALM W., HILSCHMANN N.;
HOPPE-SEYLER'S Z. PHYSIOL. CHFM. 364:713-747(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-MAI CALLINE, BOTOT295.
MARQUARI M , DEISERHOFER J. , HUBER R., PALM W.:
T MAI. RTOL. 141:369-391(1980).
                                                                                                                                   122 122
122 AA; 13166 MW; D68B085E CPC32:
                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
1G HEAVY CHAIN V-III REGION (KOL).
                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMUNOGLOBULIN V REGION; 3D-STRUCTURE.
                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE, AND DISULFIDE BONDS.
                                                                                                                                                         Query Match
Best Local Similarity 64.0%;
Matches 80; Conservative
                                                                                                                 IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MARQUAKA....
J MOL HIOL. 141.364-11-19 PIR, A02055, GHUKL.
PDB; 2FB4; 12-JUL-89.
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126
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SEQUENCE
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Best Local Similarity 66.4%; Pred. No. 3 196-110;
Matches 83, Conservative 20; Mismatches 18: Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 636; DB 5; Length 126;
Pred, No. 2.51e-111;
18; Mismatches 20; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVQLLESGGGVVQPGRSLRLSCAASGFTFKTYGMHWVKQAPGKGLEWVAGISFTGSNOYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 40AM STANDARD, FRT; 121 AA.

H43.2-UMAN STANDARD, FRT; 121 AA.

21-JUL-1986 (REL 01, CREATED)

21-JUL-1986 (REL, 01, LAST SEQUENCE UPDATE)

21-JUL-1986 (REL, 01, LAST ANNOTATION UPDATE)

IG HEAVY CHAIN V-III REGION (HIL).

HOMO SAPIENS (HUMAN).

EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA: MAMMALIA; EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYRROLIDONE CARBOXYLIC ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.1%; Score 636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKT;
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nes 87; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            1 qvqlvqsgqgvvqpgrslrlscaasgftfsrytihwvrqapqkglewvavmsybgbbkhy 60
                                                                                                                                                                                                                                                                                                                                                    6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 1 EVQLLESGGGVVQPGRSLPLSCAASGFTFKTYGMHWVPQAPGKGLEWVAGISFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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EUKARYOTA; METAZOA; CHOPDATA; VEPTERRATA; TETPAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                             EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IG HEAVY CHAIN V-II PEGION (VH26)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 117,
                                                                                                                                                                                                                                                                                                                          Length 119
                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
                                                                                                                                                                                                                                                               PYRROLIDONE CAPROXYLIC ACID
                                                                                                             MEDLINE: 77070269.
PONSTINGL H., HILSCHMANN N.;
HOPPE-SEYLEP'S Z. PHYSIOL CHEM. 357:1571-1604(1976)
                                                                                                                                                                                                                                                                                                                                                 23; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MATTHYSENS G., RABBITTS T.H.;
PPRG. NATL. ACAD SCI. U.S.A. 77.6561-6565(1990)
EMBL, J00236; G553412; -
EMBL, M35415; G553422; -
EMBL, M35415; G553422; -
EMR. M2647; H3026.
IMMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                                                                                                                                                          Score 596; DB 5, LA
Pred. No. 1.67e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 578; DB 5,
Pred No. 1 51e-98;
                                                                                                                                                                                                                                                                                     119 119
119 AA; 13242 MW; 5703CA8E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 AA; 12582 MW; 15A21B2A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
10-COT-1996 (REL. 34, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PPECUPSOP V-III PEGION (VH25)
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SECUENCE UPEATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Mismatches
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Best Local Similarity 64.8%;
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Local Similarity 77.3%;
les 75; Conservative
                                                                                                                                                                                                                                                                                                                                                   81; Conservative
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                                                                          EUTHERIA; PRIMATES.
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P01764;
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SEQUENCE
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SEQUENCE
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Score 578; DB 5; Length 120;
Pred No. 1 510-98;
19; Mismatches 17; Indels 6; Gaps
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HSSP, P01772, IEGV.
IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                               HOMO SAPIENS (HUMAN).
EUKAPYOTA: METAZGA; CHORDATA; VEPTEBRATA; TETRAPODA: MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKAPYOTA: METAZOA: CHOPDATA; VERTEBRATA; TETPAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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HOPPE-SEYLER'S Z , PHYSIOL , CHEM. 356:1337-1342(1975).
PIP: ACCOUNTE OF THE C REGION IS ALSO GIVEN.
PIP: ACCOUNTE OF THE C REGION IS ALSO GIVEN.
HSSF: FC1772, 8FAB.
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                                                                                       80 gdsvkgrftisrdnskntlylqmnslraedtavyyca 116
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122 AA: 13472 MW: BECODESE CRC32;
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                                                                                                                         61 ADSVKGPFIVSPDNSPDTVFLQMSSLRLEDTAVYYCA 97
                                                                                                                                                                                                                                                                                                                                                          LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENC
21-JUL-1986 (REL. 01, LAST ANNOTATIG HEAVY CHAIN V-III REGION (BRO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG HEAVY CHAIN V-III REGION (TRO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAPPA J D , HOPPER J E ;
IMMUNOCHEMISTRY 13:995-999(1976)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE (MYELOMA PROTEIN TRO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P01762;
21-JT1-1986 (PEL. 01, CPEATED)
21-JUL-1986 (REL. 01, LAST SEDU
21-JUL-1986 (REL. 01, LAST ANNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 62.8%;
Local Similarity 65.9%;
es 81; Conservative
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                                                                                                                                                                                                                                                                         STANDAPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 77117674.
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P01766;
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SEQUENCE
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SEQUENCE
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Score 564; DB 5; Pred, No. 1.78e-95;
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116 AA; 12730 MW; F112826G CRC32;
                                                                                                    NOW_TER 120 120
SEQUENCE 120 AA, 13440 MW, 1000FFGFF CFF72)
                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1996 (REL. 01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISION TO THE COMPOSITION OF 28-33.
                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Local Similarity 67.2%;
Les 84; Conservative
                                                                                                                                         Query Match 61.2%;
Best Local Similarity 63.2%;
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                            IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A02064; M3HUGL.
HSSP; PU1607; 1FGV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE.
MEDLINE: 75059123.
WATANARE S., RAPNII
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CRYSTALLIZATION
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P01781;
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SEQUENCE
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                                                                                   1 qvqlvesgggvvqaqtslrlsctasafnlsdyamhwvrqapgkglzwvalisyggsbtyy 60
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                                                             1 EVQLLESGGGVVQPGRSLRLSCAASGFTFKTYGMHWVRQAPGKGLEWVAGISFDGSNQYY 6U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sdeb (9
 Best Local Similarity 56.8%: Pred. No. 1.51e-98;
Matches 71; Conservative 29, Mismatches 22; Indols 3, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG HEAVY CHAÎN V-III REGION (DOB).
HOMO SADIENS (HUMAN).
EUKARYOTA; METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHOPDATA; VEPTERRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 577; DB 5; Length 119;
Pred No 2 50e-98;
22; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      PYRROLIDONE CARBOXYLIC ACID.
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STEINER L.A., GARCIA PARDO A., MARGOLIES M.N.;
BIOCHEMISTRY 18:4068-4080(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                28 28
119 119
119 Aa; 12981 MW; 323A4FE1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (RFL 01, CREATED)
21-JUL-1986 (REL 01, LAST SEQUENCE UPDATE)
01-NOV-1995 (PFL 32, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                    21-JUL-1985 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                               119 AA.
                                                                                                                                                                                                                                                                                                                                                           PUTNAM F.W., LIU Y.-S.V., LOW T L.K.;
J. BIOL. CHEM. 254:2865-2874(1979)
PIR; A02056; Alhubr.
                                                                                                                                                                                                                                                                                                                                                                                                              IMMUNOGLOBULIN V REGION; GLYCOPPOTRIN
                                                                                                                                                                                                                                                                         IG HEAVY CHAIN V-III REGION (BUR).
                                                                                                                                                                                                                                                                                                                                      SEQUENCE (MYELOMA PROTEIN BUR).
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Local Similarity 63.7%;
les 79, Conservative
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58
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                                                                                                                                          118 vtvss 122
                                                                                                                                                                 121 VTVSS 125
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                                                                                                                                                                                                             HV3L_HUMAN
P01773;
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SEQUENCE
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61 ADSVKGKFIVSRDNSRDIVFLQMSSLRLEDTAVYYCATEGSPPGSIKGRYYLENWGOGTL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l evglvesggdlvgpgrslilscaasgfbfbblgmtwrgapgkglewranikzbgszzby 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 adsvkgrfaisrdnagktlylglnilrpedtafyycak-q--yiw-ngnwf-dswqqqtl 115
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Prod. No. 1.34e-94;
18; Mismatches 14; Indels 9; Gaps
                                                                                                                                                                                                                                                                                                                                                                21; Mismatches 20; Indels 5: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         1 evqlvesggdlvqpgrslrlscaasqfnfheynmhwlrqgpgkqpewvstitwnqqsvly 60\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVQELESSGGVVQFGRSLRLSCAASGFTFKTYSMHWVPLAFGKGT FWVAGTSFFGSSNOYY 60
MEDIANE R0220920.
STEINER L.A., LOPES A.D.:
BIOCHEMISTRY 18:4054-4067(1979).
I-THIS GAMMA-1 MELLOMA PROTEIN HAS A DELETION IN THE HINGE KEGION.
THERE ARE NO LIGHT-HEAVY OF INTER-HEAVY CHAIN DISULFIDE BONDS.
PIR, A02065; GIHUDB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBMITTED (JUN-1975) TO THE PIR DATA BANK.
-!- THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOHULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WATANARE S, RAPNIKOL H II, HORN J., BERTRAM J., HILSCHMANN N.:
HOPPE-SEYLER'S Z, PHYSIOL, CHEM. 354:1505-1509(1973).
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                                                                                                                                                                                                                                                                  2 vqllesggglvqpggslrlscaasgftfsasamswvrqapgkglewva-wkyengndkhy 60
                                                                                                                                                                                                                                                                                    2 VOLLESGGGVVQPGRSLRLSCAASGFIFKTYGMHWVRQAPGKGLEWVAGISFD-GSNQYY 60
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE, 81234548.
BOTHWELL A.L.M., PASKIND M , PETH M , IMANISHI-KAPI T , PAJEWSKY K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG HEAVY CHAIN V PEGION (MOPG 21)
D SEGMENT.
                                                         HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VEFTEBFATA: TETFAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUS MUSCULUS (MOUSE).
EUKAPYOTA: METAZOA, CHOPDATA; VERTEBPATA, TETFAPODA, MAMMALIA.
                                                                                                          MEDLINE; 75046755.
CAPRA J.D., KEHOE J.M.;
PROC NATL ACAD. SCI. T. S.A. 71.4032-4035(1974).
-!- THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA GLOBULIN
                                                                                                                                                                                                                         Length 119;
                                                                                                                                                                                                                                            29; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    P01783;
21-JUL-1986 (PEL 01, CPEATED)
21-JUL-1986 (REL 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PPECURSOR V REGION (MOPC 21) (FRAGMENT).
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                                                                                                                                                                                                                       Score 557; DB 5;
Pred. No. 5.08e-94;
                                                                                                                                                                                           NON_TER 119 119
SEQUENCE 119 AA; 12858 MW; 1CE0116C CRC32;
                          21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-III PEGION (LAY).
119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JH4 SEGMENT.
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NATURE 265:299-304(1977).
EMBL; J00522; G195055; -.
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMUNOGLOBULIN V REGION: SIGNAL
                 21-JUL-1986 (REL. 01, CREATED)
                                                                                                                                                                                                                        Query Match
Best Local Similarity 59.0%;
Matches 72; Conservative
                                                                                                                                                                    HSSP; P01772; 11GM.
IMMUNOGLOBULIN V REGION.
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STANDARD;
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HSSP; P01607; 1FGV.
                                                                                                                                                              PIR; A02058; M3HULY.
                                                                              EUTHERIA; PRIMATES.
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HV3N_HUMAN
                                                                                                   SEQUENCE.
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DISULFID
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CONFLICT
CONFLICT
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60 yadsyngrfiisrndsknilyllmnslgarbialyycardagpy--ysptff-abygggt 116
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                                                                                                                                                                                                                                                            77 adtvkgrftisrdnpkntlflgmtslrsedtamyycarwgn-y-py---yamdywgggts 131
                                                                                                                                                                                                                                                                                     61 ADSVKGRFIVSRDNSRDIVFLQMSSIRLEDTAVYYCATEGSPRGSTKGRYYLENWGQGTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 evgllesggglvqpggslrlscaasgftfsssamswvrqapgkglewva-wkyengndkh 59
                                                                                                                                                                        17 dvglvesggglvqpggsrklscaasgftfssfgmhwvrqapekglewvayissgsstlhy 76
                                                                                                                                                                                                              1 EVOLLESGGGVVQPGRSLRLSCAASGFIFKTYGMHWVRQAPGKGLEWVAGISFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N -> D (PPOBABLY DUE TO DEAMIDATION DURING ISOLATION).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
1G HEAVY CHAIN V-III REGION (BUT).
HOMO SAPIENS (HUMAN).
EVKARYOTA: METALOR (HOFFGATA; VERTERRATA: TETRAFODA, MAMMALIA, EVKARYOTA; PPIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAPPA J.D., KEHOR J M ;
PROC. NATL. ACAD. SCI. U S.A. 71:4032-4034(1974)
-!- THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA GLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 547, DB 5, Length 119;
Prod No 9.376-92;
28; Mismatches 17; Indels
                                                                                    Length 136;
                                                                                                                             20; Mismatches 18; Indels
115 115 W -> H (IN REF. 2).
120 120 Y -> W (IN REF. 2).
136 AA; 15071 MW; 24BFDEBB CRC32;
                                                                             Score 555; DB 5;
Pred No. 1.57e+93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 AA; 12953 MW; 2A5697D2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (PEL 01, CPEATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
15 HEAVY CHAIN V-III PEGION (POM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P01767;
21-JUL-1985 (PEL. 01, CPEATED)
                                                                           Lonal Similarity 65.6%;
es 82; Consonner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match
Decal Similarity 59,34,
es 73, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P01772; 1FGV. IMMUNOSLOBULIN V PEGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A02057; M3HUPM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HV3M_HUMAN
P01774;
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SEQUENCE
CONFLICT
CONFLICT
SEQUENCE
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Ouery Match
Best Local Similarity 69.7%; Pred. No. 4.24e-91;
Matches 69; Conservative 17; Mismatches 12; Indels 1; Gaps
qq
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Search completed: Tue Feb 24 07:09:20 1998 Job time : 15 secs.

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*80 adsvkgrftisrdnskntlflqmhslraadtgvyycakdqlyfgsqspghy---wvqgtl 136
                 61 pdtvtgrftisrdnskntlylqmnslraedtavyycasliyyg-ydg-yamdywgqgtlv 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 evqllesggglvqpggslrlscaasgftfssyamswvrqapgkglewvaeisdggsytyy 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSAYGMHWVRQAPGKGLEWVAGIWFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SpA-reactive igM heavy chain clone 18/2.
SpA domain D; Ig binding region: IgM: B-cell superantigen; sAg;
superantigen, heavy chain variable region; VH3 restricted antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB, Q44840.

New engineered antibodies and fusion proteins for preventing plasmodium infection - contg. murine antibody CDR sequences, an corresp. nucleic acid, vectors and transformed cells Claim 14; Fig 9; 98pp; English.

Example 4 describes the prodn. of a high affinity humanised antibody. At amino acid position 49, the Ser of the humanised heavy chain Phizhro-3 was changed to Ala, which is the amino acid found at this position in the native murine NSF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 674; DB 9; Length 122; Pred. No. 2.72e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Mismatches 15; Indels
                                                                                                                                                                                                        Humanised heavy chain variable region Pfhz1c2-6. Monoclonal antibody. Plasmodium falciparum; CDR; complementarity determining region; fusion protein; murine, variable; light; heavy, chain, malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosenberg M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VH; protein-A; B-lymphocyte; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hurle M,
Gross MS;
                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    17 WAR-1994.

08-SEP-1993: U08435.

09-SEP-1992: US-941654.

(SMIK) SMITHKLINE BEECHAM COPP.

(USNA) US SEC OF ARMY.

(USNA) US SEC OF NAVY.

(USNA) US SEC OF NAVY.

SAdoff UC, Sylvester DR, Gross MPI: 94-101115/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R54784 standard; peptide; 125 AA.
                                                                                                                                                           R50315 standard; Protein; 122 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 72.8%;
Best Local Similarity 75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-OCT-1994 (first entry)
                                                                                                                                                                           R50315;
05-OCT-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>115-969936</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-MAY-1994.
29-OCT-1993; U10555.
30-OCT-1992; US-9699
                                                                                                                                                                                                                                                                                                      Misc_difference 49
                                                             137 vtvt 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 tvss 122
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                                                                                              120 VTVS 123
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                                                                                                                                                                                                                                                                         Synthetic.
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61 adsvkgrftisrdnslntlylqmnslraedtavyyctkqqvlyyg-sgsyhwfdpwgqqt 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SDSVKGRFTVSPDNSPNTLFLQMNSLPPEDTAVYYCAT-FVLFGSTKGRYY-LENWGQGT 118
Silverman GJ;
WPI: 94-16/1207/20.

WPI: 94-16/1207/20.

Stimulating prodn. of variable region gene family restricted antibodies - through B-cell super-antigen vaccination bisclosure: page 66: 130pp: English a fragment of SpA D domain that specifically binds the Fab portion of variable region restricted antibodies. The SAG is used to enhance production of VH; sepecially VH3, restricted Abs. During attempts to identify sAgs, as sequences (FS4784-801) of H chains from Ig reactive with mod-SpA, and as and DNA sequences (F74802:), Qf4402-56) of VH regions of SpA binders obtained from combinatorial libraries were determined. IgM protein 18/2 derives from the germline configuration of VH gene
                                                                                                                                                                                                                                                                                                                                                                       1 evgllesgggglvqpggslrlscaasgftfssyamswvrqapgkglewvsaisgsggstyy 60
                                                                                                                                                                                                                                                                                                                                                                                                        1 EVOLLESGGGVVOPGPSLPLSCAASGFTFSAYGMHWVPQAPGKGLEWVAGTWFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                13; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium infection - confg. murine antibody CDR sequences, corresp. nucleic acid, vectors and transformed cells claim 5, F19 6, 98pp. English.

Naturally-occurring (Q4484.42) and synthetic (Q44825.28) variable light chaim and variable heavy chaim sequences deribable chaim and variable heavy chaim sequences its variable chaim peptides, CDRS, functional fragments, Fab fragments, and analogs are useful in prodm. of fusion proteins, esp. engineered antibodies. These prods. are used to protect humans against plasmodium infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New engineered antibodies and fusion proteins for preventing
                                                                                                                                                                                                                                                                                            Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised heavy chain variable region Pfhzhc2-3. Ambnoclonal antibody: Plasmodium faloiparum; CDP; complementarity determining region, fusion protein; murine; variable; light; heavy; chain; malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hurle M, Rosenberg M;
Gross MS;
                                                                                                                                                                                                                                                                                            . Match 72.7%; Score 673; DB 9; 1
Local Similarity 73.8%; Pred. No. 3.26e-43;
les 93; Conservative 17; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T 15
R50312 standard; Protein; 122 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK) SMITHKLINE BEECHAM CORP. (USSA) US SEC OF ARMY. (USNA) US SEC OF NAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ... denvit Y, Hoffman S, h
Sadoff JC, Sylvester DR, G
WPI; 94-101115/12.
N-PSDB; Q44826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-OCT-1994 (first entry)
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09-SEP-1992; US-941654
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                                                                                                                                                                                                                                                           125 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= CDR3
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                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                             segments.
                                                                                                                                                                                                                                                                                               Query Match
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Pelease 2 1D John F Collins, Biocomputing Pesearch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07:04:38 1998; MaxPar time 9.94 Seconds 383.249 Million cell updates/sec Run on.

Tabular output not generated.

>US-08-844-215-4 (1-125) from US08844215.pep 921 1 EVQLLESGGGVVQPGPSLPL Title: Description: Perfect Score:

Sequence:

...IKGPYYLENWGQGTLVTVSS 125

PAM 150 Gap 11 Scoring table:

95051 seqs, 30469580 residues Searched.

Minimum Match 0% Listing first 45 summaries Post-processing:

pir53 Database:

lianni 2:ann2 3:ann3 4:ann4 5:unanni 5:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unann11 16:unann12 17:unann

Mean 41.619; Variance 120 293; scale 0 346 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No	02-00E C D04 A	recti 3.22e-	6.18e-	ω	2.28	.16e-7	6.07e-7	3.10e-7	ις.	5.96e-7	ır,	4.21e-7	บา			۲,		red	7-920 4 020-7	•
	Description	A diedo wysed	chain	chain	chain		heavy chain v	heavy chain V	heavy chain v	heavy chain -	chain	chain	heavy chain .	chain	heavy chain V	heavy chain -	chain	mu chain - hu	heavy chain V		
	ID Desc	139666	A60943 Id	H	M3HUAM Iq	E36005 Iq	M3HUGA IQ	S36278 Iq	H		H	+-	H	H	S31603 Iq			7453	F35005 Iq	51987B Id	44
	DB 1	7		7						7											
	Match Length	121	151	122	CCC	122	122	120	128	118	121	139	123	133	132	120	133	119	119	127	30.
* Ouerv	Match	76 1	74.5	74.3	74.2	73.8	73.7	73.5	73.0	72.7	72.7	72.7	72.1	٠. ن	<u>.</u>	71.8	71.8	71.4	0	70.6	_
	Score	701	686	584	683	680	619	677	672	670	670	670	964	663	662	661	661	658	650	650	75
Result	NO		73	٣	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	C

A60943 #type complete Ig heavy chain precursor V region (clone HN.14) - human

CI

RESULT ENTRY TITLE

22 659 23 647 24 645 25 646 25 647 26 644 27 648 31 648 32 643 33 638 33 638 33 638 34 638 34 638 35 636 36 647 41 631 44 631 44 631 44 631 45 636 40 634 41 631 42 634 43 638 44 631 45 634 41 631 42 634 43 638 44 631 45 634 45 636 40 634 41 631 42 634 43 638 44 631 45 634 45 634 46 631 47 634 47 634 48 631 49 631 49 631 49 631 49 631 40

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Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, R.K.B.
Eur. J. Immunol. (1992) 22.247.251
Restricted utilization of germ-line V(H)3 genes and short diverse third complementarity-determining regions (CDK3) in human fetal B lymphocyte immunoglobulin heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *superfamily immunoglobulin V region, immunoglobalin homology
                                                                                                Desai, R.; Spatz, L.; Matsuda, T.; Ilyas, A.A.; Berman, J.E.; Alt, F.W.; Kabat, E.A.; Latov, N. J. Meuroimmunol. (1990) 30.245
Molecular cloning of a human immunoglobulin heavy chain variable (V-H) region with anti-myelin-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Desai, R.; Spatz, L.; Matsuda, T.; Ilyas, A.A.; Berman, J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##cross-references EMBL:X62967
##note , the mucleofide sequence was submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80~{\rm ads}{\rm vkgrftisrdnskntiylqmnslrpedtavyycakkaapastgsgvdf-dywgggtl~138}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVQLLESGGGVVQPGRSLRLSCAASGFTFKTYGMHWVRQAPGKGLEWVAGISFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain - human
#formal_name Homo sapiens #common_name man
02-Dec-1993 #sequence_revision 25-May-1945 #text_change
                                                                                                                                                                                                                                                                                                                                                  Alt, F.W.: Kabat, E.A.; Latov, N. J. Neuroimmunol. (1990) 26:35-410
Molecular cloning of a human immunoglobulin heavy chain variable (V-H) region with anti-myelin-associated
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#formal_name Homo sapiens #common_name man
31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
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##Cross.references GDB:128528
#map_position 14q32.33-14q32.33
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                                 1 qvqlvesgggvvqpgrslrlscaasgftfssyqmlwvrqapqkglewvavlwydasnkyy \pm 0
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#formal_name Homo sapiens #common_name man
31-Aug-1980 #sequence_revision 23-Oct-1981 #text_change
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This mu chain was isolated from the plasma of a patient with
                                         #domain immunoglobulin homology #label IMM
th 122 #molecular-weight 13664 #chorksum 8338
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#length 122 #molecular-weight 13668 #checksum 7281
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Best Local Similarity 67.2%; Pred. No. 8.57e-77;
Matches 84; Conservative 27; Mismatches 11;
                                                                                                                Score 684, DB 7; ; pred, No. 6.18e-77;
heterotetramer; immunoqlobulin
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Local Similarity 74.4%;
les 93; Conservative
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#map_position 14q32.33-14q32.33
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
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                                                                                                                            #journal Proc. Natl. Acad. Sci U.S.A (1940) 87.6146-6150
Filtle Preferential utilization of conserved immunoglobulin heavy
chain variable gene segments during human fetal life.
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Ig heavy chain V-III region (Ga) - human
#formal_name Horne Sapiens #common_name man
*sequence_revision 23-001-1981 #text_change 31-De2-1996
#formal_name Homo sapiens #common_name man
21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change
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##residues 1-122 ##label FLO
This chain was isolated from a Waldenstrom's macroglobulin.
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#length 122 #molecular-weight 13156 #checksum 7775
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Biochemistry (1974) 19-2482-2499
The switch point in mu heavy chains of human IgM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.8%; Score 680; DB 7; Length 122; 74.6%; Pred No. 2.28e-75;
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                                                                                                                     Schroeder Jr., H.W.; Wang, J.Y.
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##residues 1-122 ##label SCH
##cross-references GB:M34030
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Matches 94; Conservative
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###residoss 1.120 ##label GRI
##rross-references EMBL-2188%?
FICATION #superfamily immunoglobulin V region; immunoglobulin homology
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Embleton, M.J., McCafferty, J., Baler, M.: Holliger, K.P.:
Gorick, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.P.; Winter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human anti-self antibodies with high specificity from phage display libraries.
836278
                                   61 ADSVKGRFIVSFDNSFDTVFLQMSSLFLEDTAVYYCATEGSPFGSIKGPYYLENWGQGTL 120
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19 heavy chain V reylon (anti-Sm, VH3/Dxp4/JH6) - human
#formal_name Homo sapiens #common_name man
13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                                                                                                                                                                                                                                                                                                #formal_name Homo sapiens #common_name man
03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
                                                                                                                                                                                                                                     S36278 #type fragment
Ig heavy chain V region (clone alpha-THY-23) - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary; nucleic acid sequence not shown
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Rest Local Similarity 72.6%; Pred. No. 6
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M.J.D.; Vossen, J.M.; Schuurman, R.K.B.
Eur. J. Immunol. (1992) 22:247-251
Restricted utilization of germ-line V(H)3 genes and short
diverse third complementarity-determining regions (CDR3) in
human fetal B lymphocyte immunoglobulin heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Library, October 1991 *superfamily immunoglobulin homology
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##note the nucleotide sequence was submitted to the EMBL Data
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                                                                                                                                                                                                                                                                                 61 adsvkgrftisrdnskntlylqmnslraedtavyycardnyyydssgyyyyygmdvwgg 120
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Iq heavy chain V region (M74) - human
#formal_name Homo saplens #common_name man
21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change
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02-Dec-1993 #sequence_revision 26-May-1995 #text_change
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                                #domain immunoglobulin homology #label IMM
th 128 #molecular-weight 14474 #checksum 9058
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                                                                                              Length 128;
                                                                                                                                     14; Mismatches 17; Indels
                                                                                                Score 672; DB 7;
Pred. No. 3.10e-75;
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heterotetramer; immunoglobulin
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nain - human
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S31116
                                                                                                Query Match 73.0%;
Best Local Similarity 73.4%;
Matches 94; Conservative
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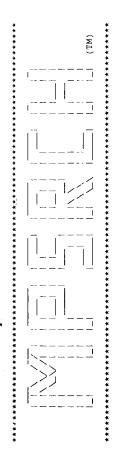
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*superfamily immunoglobulin V region: immunoglobulin homology
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                                                                      Proc. Natl. Acad. Sci. n. S. A. (1990) 87:6146-6150
Preferential utilization of conserved immunoqlobulin heavy
chain variable gene segments during human fetal life.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.;
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15; Mismatches 13; Indels 4: Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, June 1992 Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in feral liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #formal_name Homo sapiens #common_name man
22-Nov-1993 #sequence_revision 10-Nov-1995 #fext_change
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#length 139 #checksum 3756
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                                                          Schroeder Jr., H.W.; Wang, J.Y.
                                                                                                                                                                                                                                                                                                 heterotetramer; immunoglobulin
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Best Local Similarity 74.4%: Pred. No. 5
Matches 93; Conservative 15; Mismatch
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##cross-references EMBL:214204
                                                                                                                                                                                                                               1-121 ##label SCH
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CLASSIFICATION #superfamily immoort
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##molecule_type mRNA
##resid.cc
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16-Aug-1996
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1-132 ##label CUI
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Best Local Similarity 72.8%;
Matches 91; Conservative
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##residues 1133 ##label TIM
##cross-references NCBIN:54471; NCBIP:64470
##experimental_source X.linked adammadlobulinemia patients, B
##note sequence extracted from NCRI backbone
FICATION #superfamily immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION *Superfamily immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *fitle Diversity of immunoglobulin heavy chain gone segment rearrangement in B lymphoblastoid cell lines from X-linked agammaglobulinemia patients.
                                                                                                                                                                                                                                 B.D.: Voak, D.; Thorpe, S.; Hughes-Jones, N.C.; Winter, G. submitted to the EMBL Data Library, June 1993. Human antibody fragments specific for human blood group antiqens from a phage display library.
                                                                                                                                                                                                                  Marks, J D : Ouwehand, W H.; Bye, T M : Finnern, R.; Gorick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 adsvkgrftisrdnsknilylqmnslraedtavyycararsnwnyy--yyymdvwgkgit 119 \left\{\left\{\left(\left(\left(1\right)\right)\right\}\right\}\right\}
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Ig heavy chain - human (fragment)
*formal_name Homo sapiens *common_name man
06-Jan-1995 *sequence_revision Ub-Jan-1995 *text_change
16-Aug-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A49020
1g heavy chain V-11I regainn - human (fragment)
#formal_name Homo sapiens #common_name man
21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change
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Berman, J.E.; Alt, F.W.; Schuurman, P.K.
Eur. J. Immuncl. (1991) 21:2355-2353
                                                                                                                                                                                                                                                                                                                                                                                                                                                       #domain immunoglobulin homology #label IMM #length 123 #checksum 2856
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M.J.D.; Vossen, J.M.; Schuurman, R.K.B.

Pur. J. Immunol. (1992) 22:247-251
Restricted utilization of germ-line V(H)3 genes and short
divorse third complementarity determining regions (CDR2) in
human fetal B lymphocyte immunoglobulin heavy chain
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CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
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                                                                    2: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain V region - human
#formal_name Homo sapiens #common_name man
03-Mar-1994 #sequence_revision 10-Nov-1995 #fext_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in feral liver.
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02-Dec-1993 #sequence_revision 26-May-1995 #text_change
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#th 132 #m.docglar-weight 14696 #.hocksum
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      Length 133;
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Score 663; DB 7; Length 133
Pred. No. 5.83e-74;
15; Mismatches 15; Indele
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##molecule_type mRNA
##residues 1-120 ##label RAA
##rcoss-references EMBL: X62961
##note the nucleotide sequence was submitted to the EMBL Data
Library, October 1991
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                       Query Match
71.8%; Score 661; DB 7; Length 120;
Best Local Similarity 76.0%; Pred No 1 12e-73;
Matches 95; Conservative 13; Mismatches 12; Indels 5; Gaps 3;
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                                       preliminary; nucleic acid sequence not shown; translation not shown
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rearrangements.
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Pelease 2 1D John F. Collins, Biocomputing Pesearch Unit Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07:37:11 1998; MasFar time 2.42 Seconds 186.065 Million cell updates/sec Run on:

Tabular output not generated.

(1-125) from USO8844215.pep 921 >US-08-844-215-4 Description: Perfect Score:

IKGRYYLENWGQGILVIVSS 125 1 EVQLLESGGGVVQPGRSLPL Sequence:

PAM 150 Gap 11 Scoring table:

56402 seqs, 5095871 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued Database:

1:back1 2·51 3·52 4·53 5·54 6·55 7·56 8·pcT91 9·pcT91 10:pCT92 11:pCT93 12:pCT94 13:pCT95 14:pCT96 Mean 28.138; Variance 145.429; scale 0.193 Statistics:

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

on Pred. No	76, Application 1.80e-44 22, Application 1.70e-43 29, Application 1.70e-43 20, Application 1.70e-43 21, Application 6.27e-43 21, Application 6.27e-43 21, Application 1.80e-41 21, Application 1.80e-41 21, Application 1.80e-41 21, Application 1.80e-41 22, Application 1.80e-41 23, Application 6.88e-41 24, Application 6.88e-41 25, Application 6.88e-41 26, Application 6.88e-41 27, Application 6.88e-41 28, Application 6.88e-41	Applicatio 1 400-4
Description	sociones soc	30301.508
ID	US-08-331 US-08-259- US-08-468- US-08-478- US-08-478- PCT-US93-1 PCT-US93-1 PCT-US93-1 PCT-US93-1 PCT-US93-1 US-08-271- US-08-271- US-08-271- US-08-271- US-08-271- US-08-271- US-08-271- US-08-271- US-08-275- US-08-275- US-08-275- US-08-275-	08-02
Length DB	119 120 141 141 161 162 112 162 162 163 163 163 163 163 163 163 163 163 163	
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Score	000 000 000 000 000 000 000 000 000 00	621
Result No.		C1

23 658 67.1 125 13 PCT-USS5-0 Sequence 74, Applicati 2 456-40 25 618 67.1 125 13 PCT-USS5-0 Sequence 77, Applicati 2 456-40 25 618 67.1 125 7 US-0-276 Sequence 77, Applicati 2 456-40 26 618 67.1 125 7 US-0-276 Sequence 77, Applicati 2 456-40 29 618 66.7 130 7 US-0-376 Sequence 79, Applicati 2 456-40 29 618 66.6 130 7 US-0-376 Sequence 79, Applicati 1 176-40 29 618 66.6 130 7 US-0-376 Sequence 70, Applicati 1 176-40 20 618 66.6 130 7 US-0-376 Sequence 70, Applicati 1 176-39 21 60.6 6.1 120 11 PCT-USS3-1 Sequence 80, Applicati 1 176-39 22 60.6 6.1 120 11 PCT-USS3-1 Sequence 80, Applicati 1 176-39 24 60.9 66.1 120 11 PCT-USS3-1 Sequence 80, Applicati 1 176-39 25 60.0 66.1 120 11 PCT-USS3-1 Sequence 80, Applicati 1 176-39 26 60.0 66.1 120 11 PCT-USS3-1 Sequence 80, Applicati 1 176-39 27 60.0 66.1 120 11 PCT-USS3-1 Sequence 80, Applicati 1 176-39 28 60.0 66.1 120 11 PCT-USS3-1 Sequence 80, Applicati 1 176-39 29 60.0 66.1 120 11 PCT-USS3-1 Sequence 80, Applicati 1 176-39 29 60.0 66.7 122 1 PCT-USS3-1 Sequence 80, Applicati 1 176-39 29 60.0 66.7 122 1 PCT-USS3-1 Sequence 80, Applicati 1 176-39 29 60.0 66.7 122 7 US-0-84-5 Sequence 80, Applicati 1 176-39 29 60.0 66.7 122 7 US-0-84-5 Sequence 80, Applicati 1 176-39 20 60.0 66.7 122 7 US-0-84-5 Sequence 80, Applicati 1 176-39 20 60.0 66.7 122 7 US-0-84-5 Sequence 80, Applicati 1 176-39 20 60.0 66.7 122 7 US-0-84-5 Sequence 80, Applicati 1 176-39 20 60.0 66.7 122 7 US-0-84-5 Sequence 80, Applicati 1 176-39 20 7 US-0-84-46 STANDARD, PRT7, 119 AA. 20 7 US-0-84-46 STANDARD, PRT7, 119 AA. 20 8 Sequence 46, Application US/08331398A 20 8 Sequence 46, Application US/08331398A 21	OPERATING SOFTWARE: CUFFELL APPLICATION FAILS CLASSTFICATION FRICK APPLICATION PRICK APPLICATION DATE FILING DATE FILING DATE FILING DATE FILING DATE FILING TON THE FILING TON T

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                                                                                                                                                                                                                                                                   1 EVQLLESGGGVVQPGRSLRLSCAASGFTFKTYGMHWVRQAPGKGLEWVAGISFDGSNQYY 60
                                                                                                                                                                                                                          6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGIJSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF KODENT
TITLE OF INVENTION: ANTIRODIES
                                                                                                                                           LOCATION: 1..119
OTHER INFORMATION: /note- "Human fetal immunoglobulin of the Information: 56P1/CL Variable Heavy chain (V'H)"
NCE 119 AA; 13279 MW; 79818 CN;
                                                                                                                                                                                                72.6%; Score 669; DB 7; Length 119; 75.2%; Pred. No. 1.80e-44; vative 16; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sughrue, Mion, Zinn, Macpeak & Seas
                                                                                                                                                                                                                                                                                                                                                                                                               120 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
HP 9000/700 Workstation
                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 35, Application US/07942245 Patent No. 5639641 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 35, Application US/07942245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (202) 293-7060
(202) 293-7860
   TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: SEQUENCE CHAPACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: UNIX
                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             United States 37-3202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          522
                                                               119 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                  Local Similarity 75.2%;
nes 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Zivv
                                                                                                                                    NAME/KEY: Protein
                                                                           amino acid
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US-07-942-245-35
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                                                                 LENGTH:
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Ostberg, Lars G. WENDER OF HUMAN MONOCLONAL PRODUCTION PROPULATION ANTIBODIES SPECIFIC FOR HEPATITIS H SURFACE ANTIG
                                                                                                                                                                                                                          61 ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCARDRKDWGW--A-1,F-1,YWGOGT1, 116
                                                                                                                                                                                                                                           1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
                                                                                                                                                                                   4; Gaps
                                                                                                             Ouery Match 72.3%; Score 666; DB 7; Length 120: Best Local Similarity 74.2%; Pred. No. 3.16e-44; Matches 92; Conservative 15; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: Twomsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                    141 AA.
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                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08259372A Patent No. 5565354 GENERAL INFORMATION:
                                                                          MOLECULE TYPE: peptide
JENCE 120 AA; 13421 MW; 78517 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08259372A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFFLICATION NUMBER 18,708,7
FILING DATE: 14-10N-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/16
FILING DATE: 21 AFR 1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FITTN
          INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                        120 amino acids
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FILING DATE: 11-MAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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OPERATING SYSTEM:
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                                                     amino acid
                                                                    linear
6491103
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                                                                    TOPOLOGY
                                                                                                                                                                                                                                                                                         117 VTVS 120
                                        LENGTH:
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 TELEX:
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                                                        TYPE:
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FILING DATE: 21-AFR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IIS 07,676,036
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                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                            NAME: Smith, William M. REGISTRATION NUMBER: 30,223 PEFEPENCE/DOCKET NUMBER: 118
                                                                                                                                                         APPLICATION NUMBER: US OF FILING DATE: 05-SEP-1986 ATTORNEY/AGENT INFORMATION:
                                 27-MAR-1991
                                                                                                                                                                                                                                                                                      141 amino acids
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COMPUIER REALABLE FORM:
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                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                              linear
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APPLICANT: OSLÒBETY, LAIS G.
ITTLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
TITLE OF INVENTION: ANTIRODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIG
                                                                                                                                                                                                                                                                                                                         61 ADSVKGRFIVSRDIVELOMSSLRLEDTAVYYCAIEGSPFGSIKGRYYLENWGGGIL 120
                                                                                                                                                                                                                                                                                                             80 ADSVKGRFTISRDNSKNTLFLQMHSLRAADTGVYYCAKDQLYFGSQSPGHY---WVQGTL 136
                                                                                                                                                                                                                                                                 20 QVQLVESGGGVVQPGRSLBLSCAASGFTFSRYSMHWVBQAPGKGLEWVAVISYDGSNKWY 79
                                                                                                                                                                                                                                          3; Gaps
                                                                                                                                                                                                                                                                                     1 EVQLLESGGGVVQPGRSLPLSCAASGFTFKTYGMHWVPQAPGKGLEWVAGISFDASNLYY 60
                                                                                                                                                                                                                   Score 657; DR 6; Length 141;
Pred. No. 1.70e-43;
9; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 941113834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPEPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Pelease #1 0. Version #1 30
CURRENT APPLICATION DAIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
FILING DATE. 31-0CT-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER- US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER- 30,223
REPERENCE/POCKET NUMBER- 11823-50-7
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBEP: US 08/250,372
FILING DATE: 14.JUN-1994
APPLICATION NUMBER: US 07/871,426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JUN-1994
UMBER: US 07/871,426
                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/468,671
06-JUN-1995
                                                                                                                                                                                 MOLECULE TYPE: protein
FENCE 141 AA; 15613 MW; 114738 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08468671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08468671 Patent No. 5648077
                                                                                                   TELEPHONE: (415) 325-2400
TELEFAX. (415) 575-0300
INFORMATION FOR SEQ. ID NO. 2
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                             STANDAPP;
                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.2%;
Matches 94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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US-08-468-671-2
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                                                                                                                                                                                               SEQUENCE
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Query Match 71.3%; Score 657; DB 7; Length 141;
Best Local Similarity 75.2%; Pred. No. 1.70e-43;
Matches 94; Conservative 9; Mismatches 19; Indels 3; Saps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EVQLLESGGGUVVQPGRSLPLSCAASGFTFKTYGMHWVPQAPGKGLEWVAGISFDGSNQYY 60
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Patent No. 5681722
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
ROWMON, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
FILLE OF INVENTION:
FILLE OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUPNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                         11823-50-7
                                                                                                                       APPLICATION NIMBER. IIS 07/392,754
FILING PAPE: 11-MAY-1988
PRIOR APPLICATION PATA:
APPLICATION NIMBER: IIS 05/925,196
FILING DATE: 31-OCT-1986
APPLICATION DATA:
APPLICATION NAME:
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-UNN-1990
PRIOR APPLICATION DATA
APPLICATION NUMBER: US 07/;92,754
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JENCE 141 AA, 15613 MW; 114738 CN;
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VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ADSVKGRFTISPDDSKNTLYLQMNSLRAEDTAVYYCAKGQVLYYG-SGSYHWFDPWGQGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVQLVESGGGLVQPGRSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVXAISGSGGSTYY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 652; DB 7; Length 125; Pred. No. 4.32e-43;
                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039 FILING DATE: US/01/01/1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 AA.
                                                                                                                                                                                                                                                                                                           012712-160
                                                                                           CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
                                                                                                                                                                                                                FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735.064
FILING DATE: 25-UJL-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
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ICE 125 AA; 13543 MW; 93321 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application PC/TUS9310555.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                               NAME: Teskin Esq., Robin L. REGISTRATION NUMBER: 35,030 REFERENCE/DOCKET NUMBER: 011
                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 99: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                  SS: not relevant not relevant
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                                                                                                                                                                                                                                                                                                                                                                                        : 125 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.88,
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hes 88; Conserv
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                                                                                                                                                                            FILING DATE:
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APPLICANT: SILVEMAN, GREGG J.
TITLE OF INVENTION: METHOF FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
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                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                       E: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 AA.
                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER FP-2630
TELECOMMUNICATION INPORMATION:
TELEPHONE: (619) 455-5100
INFORMATION FUK SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
                                                                                                                                                                        UMBER: PCT/US93/10555
29-OCT-1993
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125 AA; 13612 MW; 90592 CN;
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                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                  NAME: Howells, Stacy L. REGISTRATION NUMBER: 34,842
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                                                                                                                                                                                                                                                                                                                                                              single
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NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                               APPLICATION NUMBER:
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                                                 Los Angeles
California
                                                                                                                                          OPERATING SYSTEM:
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                           ADDRESSEE:
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                                                                           COUNTRY:
                                                                STATE:
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STATE:
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TITLE OF INVENTION: METHOD FOR STIMILATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIRODIES
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                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYZHA: PC-DOS/MS-DOS
SOFTWARE: Patentin Pelease #1.0, Version #1.25
CUPPENT APPLICATION DATA:
     AUDRESSEE: Spensley Horn Jubas & Lubitz
STRRET: 1880 Century Park East - Suite SON
CITY: Los Angeles
STATE: California
COUNTRY USA
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29-0CT-1993
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ICE 125 AA; 13612 MW; 99692 CN;
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                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34.842
REFERENCE/COCKET NUMPER: FD-24
TELECOMMUNICATION INFORMATION
TELEPHONE: ($19) 455-5100
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INFORMATION FOR SEQ ID NO. 5
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
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NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
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CLONE: KIM
PRAFITOT
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                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 68.8%,
                                                                                                                                                                                                                                                                                                                                                                    70.6%;
                                                                                                                                APPLICATION NUMBER:
FILING DATE: 29-00T
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                      86; Conservative
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                                                                                                                                                                                                                                                                                linear
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61 ADSVKGPPIVSPDNSP)TVFTQMSSIPLEDTAVYYCATEGSPFGSIKGPYY-LENWGQGT 119
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Pred No 1 10c-42;
18, Mismatches 18, Indols 2: Gaps
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COMPUTER: IRM PC compatible
COMPUTER: SYSTEM: PC-DGS/MS-DGS
SOFTWARE: Patentin Pelease #1 0, Version #1.25
CUPRENT APPLICATION DATA:
                                     CORRESPONDENCE ADDRESS:
ADDRESSEE Spensloy Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
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TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
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FILLING DATE 29-0CT-1993
CLASSIFICATION
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F.G.
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ADDRESSEE: Genealeach, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
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LOCATION: 1 .125
NCE 125 AA; 13464 MW: 94507 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
PEGISTATION NUMBER- 34,842
PEFFERENCE/DOCKET NUMBER-
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 455-5100
INFORMATION FOR SED ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 69 8%;
Matches 88, Conservative
NUMBER OF SEQUENCES.
                                                                                                                                                                                           Los Angeles
California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLLESGGGVVQPGRSLRLSCAASGFTFKTYGMHWVRQAPGKGLEWVAGISFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 641; DB 11, Length 122;
Pred. No. 3.37e-42;
16; Mismatches 16; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Recombinant Antibodies for Human Therapy TUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE. BURNS, DOANE, SWECKEP & MATHIS STREET: 699 Prince St.
                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                             PCI/US92/05126
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122 AA; 13077 MW; 86439 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 94, Application US/08478039
Patent No. 5681722
GENERAL INFORMATION:
APPLICANT: Newman, Roland A. APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 94, Application US/08478039
                                                                                                                                                                                                                               07/934373
                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
                                                                                     SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA
APPLICATION NUMBER: PCT/US93
                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 70 TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                         TELEFAX. 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                        15-JUN-1992
                                                                                                                                                                                                                                           FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         : 122 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD:
                                                                                                                           19930820
                                                                                                                                                                                                                                                                                                                                                                                                                                 69.6%;
Local Similarity 72.0%;
les 90; Conservative
                                                                                                                                                                         FILING DATE: 14-JUN-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: F
                                                                                                                                                                                                            FILING DATE: 15-JUN-7
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                  APPLICATION NUMBER:
          STATE: California
                                                                                                                                        CLASSIFICATION:
                        USA
                                                                                                                              FILING DATE:
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US-08-478-039-94
                                  94080
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                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                        COUNTRY:
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61 ADSVKGRFTISRDDSNNTLYMGMNSLRAEDTAVYYCARDRVAVYASVFFIDSFDIWGOGT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVXV1SYINGSNEYF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 69.3%; Score 638; DB 7; Length 123; Best Local Similarity 69.1%; Pred. No. 5.89e-42; Matches 85; Conservative 20; Mismatches 17; Indels
                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/478.039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 AA.
                                                                                                                                                                  APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-5UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING TANG TANG TANGER: US 07/912,292
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATE: 23-MAP-1942
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/71
ATTORNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: TESKIN ESG., ROBIN L. REGISTRATION NUMBER: 35,030 REFERENCE/PACKET NUMBER: 012712-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNET/AGENT INFORMATION:
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Patent No. 5565332
GENERAL INFORMATION:
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                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SS: not relevant not relevant
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                                                                                                                                                                                                                                                                                                                         FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 23-MAP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 123 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     703-836-6620
                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 703 -836-2021
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POSITION IN GENOME:
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHROMOSOME/SEGMENT:
CITY: Alexandria
                                                     22313-1404
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                                     USA
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                                                                                                            COMPUTER:
                                   COUNTRY:
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STATE
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AC
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DT
                                                                David W. Clough, Marshall O'Toole Gerstein Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLVESGGGVVQPGPSLPLSCAASGFTFSSYAMHWVPQAPGKGLEWVAVISYDGSNKYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Caps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ADSVKGRFIVSRDNSRDTVFLQMSSLRLEDTAVYYCATEGSPFGSIKGPYYLENWGGG 119
      APPLICANT: JESPERS, Laurent Stephane Anne Therese APPLICANT: WINTER, Gregory Paul TITLE OF INVENTION: Production of chimeric antibodies - a TITLE OF INVENTION: combinatorial approach NUMBER OF SEQUENCES - 144
CORRESPONDENCE ADDRESS:
                                                                                                                                      MEDIUM TYPE: Florpy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1 0, Version #1 25 (EPO)
CURPENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 637; DB 6; Length 116;
Pred. No. 7.10e-42,
16; Mismatches 13; Indels
                                                                                  6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 AA
                                                                                                                                                                                                                                                                                                                                                                                           28111/31960
                                                                                                                                                                                                                                                                                                                                      APPLICATION NIMBER PCT/GR42/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36, 107
REPERENCE/POCKET NUMBER: 28, 117, 3196(
                                                                                                                                                                      23-SEP-1992
N: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: por zero
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                                                                                                                                                                                                                  PRIOR APPLICATION DATA.
APPLICATION NUMBER. GR 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA.
APPLICATION NUMBER: GR 9120377.8
FILING DATE: 25-SEP-1991
                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER GR 9206318 9
FILING DATE: 24-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
UENCE 116 AA; 12678 MW; 72426 CN;
                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 141:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 116 amino acids
amino acid
APPLICANT: BAIER, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHAPACTERISTICS
                                                                                                                                                                                                                                                                                             FILING DATE: 24-MAR-
PRIOR APPLICATION DATA-
APPLICATION NUMBER:
FILING DATE: 24-MAR-
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Best Local Similarity 73./*.
87; Conservative
                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                     Illinois
                                                                             STREET: bocc
                                                                                                                       50505-5402
                                                                                                                                                                                                  FILING DATE: 23 CLASSIFICATION:
                                                                                                              USA
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PCT-US93-08435-43
                                                                 ADDRESSEE:
                                                                         ADDRESSEE .
                                                                                                              COUNTRY:
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APPLICANT: U.S. Government, Secretary of APPLICANT: the Army TITLE OF INVENTION: Novel Antibodies for Conferring Passive TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man CURPESPONDENCES: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PDIVIGRFIISEDNSKNILYLAMNSLMAEDIAVYYGASLIY-YG-YDG-YBRYWGGIL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 512, DB 11, Longth 122;
Pred. No. 1.80e-41;
15; Mismatches 18; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVQLLESGGGVVQPGPSLPLSCAASGFTFKTYGMHWVPQAPGKGLEWVAGISFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pelease #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                   SmithKline Beecham, Corporation I S. Government, Secretary of
                                                                                                                                                                                                                                                                               Howson and Howson
x 457, 321 Norristown Foad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME. Bak, Mary E.
REGISTRATION NUMBER: 31,215
PEFERENEZPONKET NIMREP. SRC P50107
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US93/08435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
AITGENEY/AGENT INFORMATION:
                                        Sequence 43, Application PC/TUS9308435 GENFPAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application PC/TUS9308435
Sequence 43, Application PC/TUS9308435.
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SEQUENCE 122 AA; 13313 MW; 87403 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (215) 540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (215) 540-5818
INFOPMATION FOR SEQ ID NO: 4
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 122 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READARLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.2%;
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                 STREET: Box 457, 34 CITY: Spring House
                                                                                                                       APPLICANT: the Navy APPLICANT: U S. Gov.
                                                                                                                                                                                                                                                                     ADDRESSEE: HOWSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                19477
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                                                                                                          APPI ICANT
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Sequence 14, Application PC/TUS9308435
GENERAL INFORMATION:
APPLICANT: Smithfile Beecham, Corporation
APPLICANT: U.S. Government, Secretary of
APPLICANT: the Navy
APPLICANT: the Army
APPLICANT: Immunity Against Infection by a Pathogen in Man
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PDIVTGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCASLIY-YG-YDG-YAMDYWGQGTL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVOLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSEISDGGSYTYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVQLLESGGGVVQPGRSLRLSCAASGFTFKTYGMHWVPQAPGKGLEWVAGISFDGSNOYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 70.4%; Pred. No. 2.62e-41; Length 122;
Matches 88; Conservative 16; Mismatches 18; Indels 3;
                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM. PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1 0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REPRENCE/DOCKET NUMBER: SBC P50107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEPHONE: (215) 540-5818
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                   E: Howson and Howson
Box 457, 321 Norristown Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPT:
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US93/08435
                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
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Patent No. 5565332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
122 AA; 13329 MW; 88138 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 118, Application US/08211202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDAPD:
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                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA
                                                                                                                                       NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inear
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US-08-211-202-118
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                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                              STATE:
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1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
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ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray & ADDRESSEE: Borun
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HOOGENBOOM, Hendricus Renerus Jacobus Matteus
                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Vorsion #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER. US/C8/211 2000
FILING DATE:
            APPLICANT: BAIER, Michael
APPLICANT: JESPERS, Laurent Stephane Anne Therese
APPLICANT: WINNER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies
TITLE OF INVENTION: combinatorial approach
NUMBER OF SQUENCES: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 628: DR 6: Length 98;
Pred. No. 3.80e-41;
11; Mismatches
                                                                                                                  6300 Sears Tower, 233 South Wacker Drive
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FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                              FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING LATE: 24-MAR.1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
                                                                                                                                                                                                                                                                                   PULDA DESTITUTION DATA:
PRIOR PELICATION NUMBER. GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR PRILICATION DATA:
APPLICATION NUMBER: GB 9120377.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
JENCE 98 AA; 10838 MW; 50043 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: David W. Clough
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 24-MAR-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: F
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Best Local Similarity 83.5%;
                                                                                                                                                                                  COMPUTER READABLE FORM:
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                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                              Illinois
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                                                                                                                                    Chicago
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      APPLICANT:
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APPLICANT: SmithKline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Navy
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Army
TITLE OF INVENTION: Novel Antibodies for Conferring Passive
TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
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Best Local Similarity 70.4%; Pred. No. 3.80e-41;
Matches 88; Conservative 15; Mismatches 19; Indels 3; Gaps
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COMPUTER PEADAPLE FORM.
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
FILING DATE:
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REGISTRATION NUMBER: 31,215
PEPERENCE/DOCKET NUMBER: SEC P50107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEPHONE: (215) 540-9200
INFORMATION FOR SEC ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Howson and Howson
STREET Box 457, 321 Norristown Road
CIIY: Spring House
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                       Sequence 12, Application PC/TUS9308435 GENERAL INFORMATION:
                                                                                                                   Sequence 12, Application PC/TUS9308435.
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MOLECULE TYPE: protein
SEQUENCE 122 AA; 13370 MW; 87746 CN;
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amino acid
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STATE:
01-JAN-1909
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Search completed: Tue Feb 24 07:37:23 1998 Job time : 12 secs.

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Release 2.1D John F. Collins, Biocomputing Fesearch Unit Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07-10:11 1999, MasPar time 7.49 Seconds 231.859 Million cell updates/sec Run on:

Tabular output not generated

>US-08-844-215-4

Description: Perfect Score: Sequence:

TRGRYYLENWGQGTLVTVSS 125 (1-125) from USG8844215.pep 921 1 EVQLLESGGGVVQPGRSURL.

PAM 150 Gap 11 Scoring table:

111726 seqs, 13889129 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-genesed30 Database:

| part| 2 part2 3 part3 4 part4 5.part5 5 part5 7.part7 8:part6 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21.part21 22:part20 23:part23

Mean 30.277; Variance 155.246; scale 0.195 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
	600	7.4.0	100		520161		
4 1	0 1		707		TOTOCK	seducine of the neavy	0 t - 2 c T - T
7	581	73.9	123	23	W13531	Anti-melanoma antibod	6 150-45
m	680	73.8	206	7	P12134	ORF 3 of 4B9 human MA	7.43e-45
4	677	73.5	123	23	W15534	Anti-TGF beta-1 scFv	1 300-44
Ŋ	674	73.2	4	51	R75393	Anti-interleukin-1-al	2.290-44
٥	699	72.6	113	α: • •	R95216	Human foetal immunoq1	5.850-44
7	668	72.5	123	23	W15535	Anti-TGF beta-1 scFv	7.07e-44
œ	999	72 3	115	4	P22571	Heavy chain VH3 5 fro	1 036-43
6	666	72 3	150	17	P52054	Heavy chain variable	1.036-43
10	657	71.3	141	19	W01522	Monoclonal antibody P	5.57e-43
11	657	71.3	141	23	W24984	Monoclonal antibody P	5.57e-43
12	653	70.9		23	W13524	Anti-melanoma antibod	1.186-42
13	651	7.07	143	σ	R54047	Sequence of the VH re	1.72e-42
14	650	7 Û E	125	C	P54788	SpA-reactive IgM heav	2 070-42
15	650	70 E		σ.	P54789	SpA-reactive IqM heav	2.076-42
16	649	70.5	123	C.	W15536	Anti-TGF beta-1 scFv	2 50e-42
17	639	69.4	11	7	P12275	Anti-human Php HAM-R	1.530-41
18	638	59.3	124	C1	W13537	Anti-melanoma antibod	1 976-41
19	638	69.3	125	σ,	P54784	SpA-reactive IgM heav	1.970-41
20	638	69.3	140	14	R89480	Anti-human IL-4 human	1 976-41

.97e-4	96	.02e-4	9-050	24e-4	e-4	. <u>66e</u> -4	1960-4	.28e-4	290-4	28e-4	540-4	.54e-4	.86e-4	.86e-4	.24e-4	.71e-4	.71e-4	71e-4	.260-4	94e-4	.75e-4	.75e-4	6-4
IL-4 hum	immunod]	MAb heavy cha	anised heary cha	vy chal	anised heavy ch	lanoma a	an anti-HBs he	i-human PhD	i-TGF beta-2 s	anised heavy c	riable region o	2-109/112-61/h1-1	-TGF beta-2 s	antibody C4.1	83	sensus	tr	region of H	SD2 hu	P bind	egion of HIV	1-HIV gp120 immu	-mbibabi
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ALIGNMENTS

/label= Fab/ EP-54654-A 16-UNN-1993. 19-DEC-1991; 3S-807300. (ALKG) AKGO NV. Crichton VZ. Haspel MV, Kobrin WFI: 93-196019/24.	
/label= CDR 3 Region /label= CH 1 224238 Region /label= Hinge 239242 Recion /label= Fab' RP-546644A 16-JUN-1992; 203827. 13-EC-1991; 95-807300. (ALKU) AKEO NV. Crichton VZ, Haspel MV, Kobrin WFI; 93-196019/24.	/label= CDR 3 Region 1122 /label= CH 1 2242 /label= Hinge 2392 Region 2392
/ Mabel = VAR	/label= VAR Region

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rrom a cancer pattern.

A process for isolating and synthesising human monoclonal anti-tumour can include as been produced. The process involves: (a) constructing at antibodies has been produced. The process involves: (a) constructing at least one fusion phage library from the peripheral blood lymphocytes (c) the phage library in a binding assay with cultured tumour cells of the the phage library in a binding assay with cultured tumour cells of the construction against normal human cells: (d) cloning the phage selected in absorption against normal human cells: (d) cloning the phage selected in absorption against normal human cells: (d) cloning the phage selected in absorption against normal human cells: (d) cloning the phage by step (b) and (c); (e) assaying the specificity of the cloned phage by ind (d) further testing the specificity of cloned phage by considering the phage with at least two types of cultured normal cells: (d) cloned phage the or cultured tumour cells derived from more than one other tumour that is to cultured tumour cells derived from more than one other tumour that is to cultured tumour cells derived from more than one other tumour cells derived from sold for isolating tumour cells derived from season sequence contains and for sudding tumour cells and therapeutic applications and for isolating tumour can the monoclonal antibodies Mabs). Since the antibodies are isolated fumour cell line can be improved by genetic manipulations.

C from fusion phage libraries, their affinity and specificity for a cultumour cell line can be improved by genetic manipulations.
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                                                                                                                                                                                                                                                                                                                                                                                                              1 EVQLLESGGGVVQPGRSLRLSCAASGFTFKTYGMHWVRQAPGKGLEWVAGISFDGSNQYY 60
human variable region heavy chains have a cysteine at this posn. i.e. Rabat posn. 59.
Sequence 192 AA;
                                                                                                                                                                                                                                                                                                                                     20 qvqlvesgggvvqpgrslrlscaasgftfssygmhwvrqapgkgldwvavisydgsneyc 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-melanoma antibody héavy chain clone V575.
Human; monoclonal antitumour antibody; peripheral blood lymphocyte;
cancer; tumouriqenesis; anticancer vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prodn. of human monoclonal anti-tumour antibodies - by screening a fusion phage library produced using peripheral blood lymphocytes from a cancer patient
                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.9%; Score 681; DB 23; Length 123; 73.6%; Fred No K 15e-45;
                                                                                                                                                                         Score 690; DB 7; Length 192;
Pred. No. 1.13e-45;
                                                                                                                                                                                                                                                               17; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T
W13531 standard; protein; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 73.6%,
                                                                                                                                                                                          Query Match
Best Local Similarity 72.8%;
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-497647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31..35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50..66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUN-1996; IB1032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;, Garen A;
97-109061/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 vtvss 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 VTVSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label - CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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18; Mismatches 12; Indels 3; Gaps

Matches

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307 adsvkgrftisrdnsrdmlyvqmnslraedtavyycakekcs qq--scysfdywqqtl 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 gyglvesgggvvgpgrslrlscaasgftfrsygmhwyrgapkglewvavissdgsydyy 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVOLLESGGGGVVOPGRSLPLSGAASGFTFKTYGMHWVPQAPGKGLFWVAGISFDGSNOYY 60
                                                                               Mismatches 12: Indels 3: Gaps
                                                             61 adsvkgrftisrdnskkntlylgmnslraedtavyycar-gipygg-nsdygmdvwdhgt 118
1 qvqlvesgggvvqpgrslriscassgftfssyamhwvrqapqkglewvavisydqsnkyy 60
                            1 EVQLLESGGGVVQPGRSLRLSCAASGFTFKTYGMHWVRQAPGKGLEWVAGTSFDGSNOYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Fig 18; 104pp; English.

This sequence is derived from the nucleotide sequence encoding the heavy chain variable region. The "x" residues represent nonsense codons. The coding sequence has been translated in all 3 reading frames (see also R1212 and R12133).

See also 011878 and 011879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MINION-1997 (first entry)
27-NOV-1997 (first entry)
Anti-TGF beta-1 scFv antibody 1-B2 VH domain.
Transforming growth factor beta-1; TGF-beta-1; human;
antibody engineering; scFv. phage display; hung fibrosis;
arterial injury; profilerative retinopathy; retinal detachment;
adult respiratory distress syndrome: liver cirrhosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligomeric immunoglobulin(s) with high avidity for antiqen(s) formed by duplicating esp. variable region of light chain of 196
                                                                                                                                                                                                                                                                   01-AUG-1991 (first entry)
ORF 3 of 4B9 human MAb heavy chain variable region; duplication;
immunoglobulin G; heavy chain; variable region; duplication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match
Local Similarity 76.0%; Pred. No. 7.43e-45;
les 95; Conservative 15.
                                                                                                                                                                                                                                                                                                                                                                                               /note= "last 3 residues of leader and variable
                                                                                                                                                                                                                                                                                                                                                                                                               region; the rest of leader is translated in
                                                                                                                                                                                                                                                                                                                   immunity; group B streptococci.
                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
244..369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W15534 standard; Protein; 123 AA.
                                                                                                                                                                                                                             T
R12134 standard; Protein; 506 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shuford WW, Harris LJ, Raff HV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BRIM ) BRISTOL-MYERS SQUIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-NOV-1989; US-432700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-NOV-1990; U06426
                                                                                                                                                                                                                                                                                                                                                                                     /label= L'V region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 91-163947/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364 vtvss 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 VTVSS 125
                                                                                                                                           119 qutvs 123
                                                                                                                                                                         120 LVTVS 124
                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09106305-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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immune and inflammatory disease

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ADSVKGPFIVSPDASPDAVFUZASSLPLEDIAVYYGATEGSPFGSIKGPYYLENWGGGTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 qvqlvesgggvvqpgrslrlscaasgftfssygmhwvrqapgkglewvavisydgsnkyy 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agent contg. antigen-binding domain of human antibody to transforming growth factor beta 1 or 2 - and nucleic acid encoding it, used to neutralise effects of TGF, \theta g for central of fibresis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used for prodn. of recombinant antigen-binding domains. These are highly specific, have low dissociation constants (pref. less than 5
                 scleroderma; vascular didease; cataract; glaucoma; scarring; glomerulonephritis; osteoporosis; immune disease; inflammation; rheumatoid arthritis; macrophage deficiency disease; macrophage pathogen infection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R75393.
04-NOV-1995 (first entry)
Anti-interleukin-1-alpha human monoclonal antibody VH segment.
Monoclonal antibody, interleukin-1-alpha, eytekine,
antiinflammatory; prophylactic; therapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 73 5%; Score 577; DB 23; Length 123; Local Similarity 73.6%, Pred. No. 1.30e-44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
post myocardial infarction; post-angioplasty restenosis;
                                                                                                                                                                                                                             07-007-1995, GE-001081.
19-JAN-1995, GE-020486.
06-007-1995, GB-020486.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                 Bacon L, Green JA, Jackson PH, Johnson KS, Pope (
Tempest PR, Thompson JE, Vaughan TJ, Williams AJ)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          k (FR) 1 (+1 to +30)"
50, 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nM) and low IC50s for neutralisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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1
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/note* "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.49
                                                                                                                                                                                      23-APR-1997
07-001-1996; 020920
                                                                                                                                                                                                                                                                                                                                                                                                             97-215360/20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; T60380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 vtvss 123
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                                                                                                                                       Homo sapiens.
GB2305921-A
                                                                                                                                                                                                                                                                                                                                                                                            Wilton AJ
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80 aesvkgrftisrdnsknilflymdslrledtamyycar-grpkmnipap--lahwyggtl 126
                                                                                                                                                                                                                                                                                                                                        The sequence represents the variable heavy chain segment of a human monoclonal antibody (HuMAb) against interleukin-1-alpha. The MAb is of subclass 1964 and binds to lymphokines/monokines with an affinity of 10(9)/M. The Mab or fragment (FV, single-chain FV, Fab or F(ab') is used in the treatment of inflammation e.g. rheumatoid arthritis, osteoarthritis and inflammatory bowel diseases, and in the treatment or psortial inflammatory bowel diseases, and in disease and tumours. The MAb or fragment can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVULLESGGGVVQPGRSLRLSGAASGFIFKIYGMHWVRQAPGKGLEWVAGLSFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 574, DB 13, Length 141;
Pred. No. 2.29e-44;
15; Mismatches 15, Indels 3: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 grglvesggggvrgpgrslrlsctasgftfsmfguhwrrgspgkglewraavsydgsnkyy
                                                                                                                                                                                                                                                                                                 Human monoclonal antibody against a human cytokine - used to mfr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R952107
16-DEC-1996 (first entry)
16-DEC-1996 (first entry)
Human foetal immunoglobulin 56pl'CL variable heavy chain.
Human foetal immunoglobulin single chain; inhibition; tumour:
Antibody; fusion protein; single chain; inhibition; tumour:
Antibody; fusion; immaniotoxin; targetting; assay;
                                                                                                                                                                                                                                                     Djossou O, Fossiez F, Garonne P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                               medicament to treat inflammation.
Claim 7; Page 44-45; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .m. 6
R95216 standard; protein; 119 AA.
R95216;
                                                                                                                  /hote= "CDP 3 (+99 to +110)"
                                                                                                                                              "JH 1 (+111 to -122)"
                                                        "CDR 2 (+50 to +66)"
86..117
"CDR 1 (+31 to +35)"
55..68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cuery Match
Best Local Similarity 73.6%;
Matches 92; Conservative
                            "FR 2 (+36 to +49)"
                                                                                    "FR 3 (+67 to +98)"
118 129
                                                                                                                                 130.141
                                                                                                                                                                                                                        (SCHE ) SCHERING-PLOUGH. (SCHE ) SCHERING CORP.
                                        .85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-OCT-1994; US-331398.
28-OCT-1994; US-331396.
28-OCT-1994; US-331397.
                                                                                                                                                                                                         23-NOV-1993; EP-402846.
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C)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 AA;
                                                                                                                                                                                                                                                    Banchereau J, Djc
WFI; 95-206937/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= CDR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= CDR 3.
                                                                                                                                                                                                                                                                                   N-PSDB; 087236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 vtfss 141
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09-MAY-1996.
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28-0CT-1994;
                                                                                                                                                               WO9514780-A.
                                                                                                                                                                             01-JUN-1995
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               Region
/note=
                                                                                                                                   Region
                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
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                                                                           Region
                                             Region
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Example 13: Figure 11A: 116pp; English.

Example 13: Figure 11A: 116pp; English.

Example recombinant DNA molecule which encodes a single chain fusion protein or antibody comprising the FV region of both the light and heavy chains of an antibody (Ab) fused together, and an effector molecule, where the fusion protein or Ab has the binding specificity of monoclonal Ab (MAb) B1, B3 or B5, can be used for the production of such fusion proteins or antibodies. The fusion proteins can be used in compositions as an immunictoxin to inhibit tumour cell growth the single chain antibody can be used to detect the presence or The single chain antibody can be used to detect the presence or patient. The antibodies are also useful as multiple targetting moleties, providing at least 2 kinds of biological activity. They can also be used in diagnostic assays and for the imaging of tumours tumours. Humanised antibodies are less immunogenic than the mouse the mouse also be used to a radiolabel and for the pathological diagnosis of tumours. Humanised antibodies are less immunogenic than the mouse make the first pathological diagnosis of the first pathological contains the mouse of the first pathological contains the mouse the first pathological contains the mouse first pathological contai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 adsvkgrftisrdnskntlylqmnslraedtavyycarr-s---a-rt-yyfdywgggtl 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ADSVKGRFIVSRDNSRDTVFLQMSSLRLEDTAVYYCATEGSPFGSIKGRYYLENWGQGTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agent contg. antigen binding domain of human antibody to transforming growth factor beta 1 or 2 - and nucleic acid encoding it, used to neutralise effects of TGF, e.g. for control of fibrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 qvelvesgggvvqpgrslrlscaasgftfssyamhwvrqapqkglewvavisydgsnkyy 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

72.6%; Score 669; DB-18: Length 119:
Best Local Similarity 75.2%; Pred. No. 5.86e-44;
Matches 94; Conservative 16; Mismatches 9; Indels 6; Caps
                                                                                                                  Single chain fusion proteins and antibodies - useful to diagnose and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-TGF beta-1 scrv antibody 31G9 VH domain.

Anti-TGF beta-1 scrv antibody 31G9 VH domain.

Transforming growth factor beta-1; TGF-beta-1; human;

antibody engineering; scrv; phage display; lung fibrosis;

arterial injury; proliferative retinopathy; retinal detachment;

adult respiratory distress syndrome; liver cirrhosis;

post myocardial infarction; post-angioplasty restenosis;

scleroderma; vascular diedesse; cataract; glaucoma; scaring;

scleroderma; vascular diedesse; cataract; glaucoma; scaring;

rheumatoid arthritis; macrophage deficiency disease;

rheumatoid arthritis; macrophage deficiency disease;
                                                                                                                                            treat cancer, specifically bind Lewis(Y) related carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnson KS, Pope AR;
                                [,ee B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Williams AJ;
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Benhar I, Brinkmann U, Fitzgerald D, Jung S,
                                       Benhar'I, Brinkmann U, Fitzgerald D, Juny
Padlan EA, Pai L, Pastan I, Willingham M;
WPI, 96-251462/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W15535 standard; Protein; 123 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JAN-1996; GB-001081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-OCT-1995; GB-020486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vtvss 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 VTVSS 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sednence
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Claim 16; Fig la(ii); 184pp; English.

This polypeptide comprises the VH domain of human screw antibody which is specific for transforming arouth factor (TGF)

beta-1. It is encoded by a gene (T66381) isolated from a large beta-1. It is encoded by a gene (T66381) isolated from a large content beta-1. It is encoded by a gene (T66381) isolated from a large content beta-1. The antigen-binding domains of human content the adverse effects of TGF beta, such as (i) promotion to counter the adverse effects of TGF beta, such as (i) promotion of fibrosis (in dermal, ocular or Keloid scarring, lung fibrosis, cofficial injury, proliferative retinopathy, retinal detachment, adult respiratory distress syndrome, liver cirrbosis, scleroderma, mycoardial infarction, post-angioplasty restensis, scleroderma, comparate disorders, cataract, glaucoma, or esp. neural scarring and glomenionephritis, also (not claimed) osteoporosis), or (ii) immune and inflammatory diseases (e.g. rheumator) artificial colds encodain antibody VH and VL can be used for prodn. of recombinant antigen-binding domains. These are highly compared to specific, have low dissociation constants (pref. less than 5 nM) sequence 123 AA; sequence 123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 adsvkgrftisrdnskntlylgmnslraedtavyycartge-ysgydtsg-velwgggtt 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ADSVKGRFIVSRDNSRDIVFLQMSSLRLEDTAVYYCATEGSPFGSIKGRYYLFNWGQGTL, 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l qvqlvqsgggvvqpgrslrlscaasgftfssygmhwvrqapqkqlewvavisydqsikyy 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pCR was used to prepare a human scFv library from RNA from white blood cells from an unimmunised donor Heavy chains from 19G and 19M antibodies were amplified separately. Four separate libraries were generated (19G-K, 19G-lambda, 19M-K and 19M-lambda). The purified scFv fragments were ligated into the phagemid pilms! for purified scFv fragments were ligated into the phagemid pilms! for prepression on the surface of id bacteriophage as quene [1] instons. The clones were then subjected to affinity selection for binding to phox:BSA by selection on tubes followed by analysis by ELISA. Of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAY-1992 (first entry)
Heavy chain VH3.5 from BSA binding scFv fragment.
Heavy chain VH3.5 from BSA binding scFv fragment; coat;
Fd; bacteriophage, gene III; llamentous; phagemid; capsid; coat;
pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
specific binding pairs; replicable genetic display package; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        wccafferty J, Pope AR, Johnson KS, Hoogenboom HKJ, Griffills AD: Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ: Winter GP, Bonnert TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Producing members of specific binding pairs - by expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
72.5%; Score 668; DB 23; Length 123;
Best Local Similarity 73.5%; Prod No 7.07e-44;
Matches 92; Conservative 15; Mismatches 16; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        recombinant host cells with a secreting replicable genetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R22571 standard; Protein; 115 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CAMB-) CAMBRIDGE ANTIBODY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-MAR-1991; GB-004744.
15-MAY-1991; GB-010549.
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Table 11; Page 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 vtvss 123
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120 AA;

Seguence

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Method of resurfacing of rodent antibodies to produce humanised antibody forms - for producing non-human antibodies with improved therapeutic efficiency by presenting human surface on V-region Example 1, Fig 4B, 230pp; English.

Modification of a rodent antibody (Ab) or fragment by resurfacing in order to produce a humanised rodent Ab can be determined by calculating homology between murine and human Ab antibody surfaces. In order to test the resurfacing approach of the invention, three humanisation experiments were set up: (1) traditional loop grafting (2) resurfacing approach using most similar chain; and (3) resurfacing approach using human sequences with most similar surface residues. The Ab used was the murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anti-N901 Ab (see R52064). Experiment 2 was carried out using the present sequence which represents the human G36005 Ab heavy chain variable present with 89 percent homology with anti-N901 Ab N901/355005 (P52055) was prepding Sequence numbering starts at 118 in the specification.
                                                                                                                                                                                                                                                                                                                                     1 qvqlvqsqgg...qpgrslrlscaasgftfssygmhwvrqapgkglewvavisydgsnkyy 60
                                                                                                                                                                                                                                                                                                                                                                               1 EVQLLESGGGVVQPGRSLRLSCAASGFTFKTYGMHWVRQAPGKGLEWVAGISFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                    61 adsvkgrftisrdhskntlylgmnslraedtanyycaktg--yssgwg-yf-dywgggt 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ADSVKGRFIVSRDNSRDTVFLQMSSLRLEDIAVYYCATEGSPFGSIKGRYYLENWGQGT 119
                                                                                                                                                                                                                                                                                                 4; Gaps
96 clones analysed, 43 showed binding to both phox:RSA and BSA. These were designated BSA binders. Thirteen of fourteen clones sequenced had the same sequence, the VH derived from a human vH3 family gene (Shown here) and the VL from a human vH4 family gene (R2552). The other was derived from a human vH4 family gene one chone bound only to phox:BSA (oxazolono bindin) in this sequence revealed a VH derived from a human vH1 family gene (R22569) and VL from a human v lambda I family gene (R2250). See also R2156.307, 309.312, R22565, R22565, R22567.81 sequence 115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-0cT-1996 (first entry)
Heavy chain variable region of human G36005 antibody.
antibody; humanised; murine; human; heavy chain; light; variable; framework region; complementarity determining region; reshaping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pedersen JI, Pees AP, Poguska MA, Searle SMJ;
                                                                                                                                                                                                                                                   Query Match 72.3%; Score 666; DB 4; Length 115; Best Local Similarity 75.6%; Pred. No. 1.03e-43; Matches 90, Conservative 15, Mismatches 10, Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modelling; surface residue; modify.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R52064 standard; Protein; 120 AA.
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                                                                                                                                                                                                                                                                                              90, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PEDE/) PEDERSEN J T. (IMMU-) IMMUNOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-1993; 307051
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diseases caused by infection with hepatitis. B have been prepared from a cell line obtained by fusing a xengeneic hybridoma designated SPAZ 4 with blood cells of a patient immunised with hopetitis P vaccine. Specific antibodies are PEI-1, ZMI-1, ZMI-2, MD3-4 and L03-3, each of these being of the IgG1 class. The present sequence is the heavy
                                                                                                                                                                                                                                                                           61 adsvkgrftisrdnskntlylqmnslraedtavyycardrkdwgw--a-lf-dywgggtl 116
                                                                                                                         Human monoclonal antibodies specific for hepatitis B surface antigen are used to treat or prevent infection of in diagnostic assays claim 4; Column 27-28; 26pp; English.

Monoclonal antibodies effective for the diagnosis and treatment of
                                                                                                                                                                                 1 EVQLLESGGGVV@P@PSLFLSGAASGFTFKTYGMHWVFQAPGKGLEWVAGISFDGSN@YY 60
                                                                 4; Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-MAR-1997 (first entry)
Monoclonal antibody PEL-1 heavy chain variable region.
Monoclonal antibody; diagnosis; treatment; infection; hepatitis B;
xenogeneic hybridoma; SPAZ 4; PEL-1; ZM1-1; ZM1-2; MD3-4; L03-3;
IgGl class, heavy chain, light chain, variable region.
Score 666, DB 17; Length 120;
Pred. No. 1.03e-43;
15; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'label - complementarity_determining_region_l
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W01522 standard; Protein; 141 AA.
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Query Match 72.3%;
Best Local Similarity 74.2%;
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= framework_region_l
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/label= V_H(III)_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= leader_sequence
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31-OCT-1986; US-925196.
11-MAY-1988; US-192754.
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27-MAR-1991, US-676036.
21-APE-1992; US-871426.
14-JUN-1994; US-259372.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= J_H4_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                               117 vtvs 120
                                                                                                                                                                                                                                                                                                                                                                                                                       121 VTVS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "CDR1"
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Example 8: Column 15-18: 25pp; English.

Example 8: Column 15-18: 25pp; English.

This is the amino acid sequence of the heavy chain variable (Vh) region this is the amino acid sequence of the heavy chain variable (Vh) region from the human monoclonal antibody (MAD) PEI-1. The MAD was generated by immunising humans with a hepatitis B virus (HBV) vaccine, isolating peripheral, blood lymphocytes (PBL) and fusing them with a mouse/human xenogeneic cell line SPAZ-4. 5 cell lines were isolated? PEI-1, ZMI-1, ZMI-2, MAD-3.4 and LO3-3. The cell lines were then tested for production of an anti-hepatitis B virus surface antigen antibody by ELISA The MADs are then purified from large scale cell culture by protein A chromatography, size separation on Sephacryl S300 gel and ion exchange
                                                                                                                                                                                                                                                                                                                                                                               08-DEC-1997 (first entry)
Monoclonal antibody PEI.1 Wh region, human; monoclonal antibody;
Heavy chain; light chain; variable region; human; mouse; fusion; senogeneic;
immunisation; hepatitis B virus; HBV; vaccine; mouse; fusion; senogeneic;
peripheral blood lymphocyte; surface antiqen; cell culture; ion exchange;
peripheral blood lymphocyte; primer; PCR; polymerase chain reaction;
chromatography; size separation; primer; PCR; polymerase chain reaction;
amplification; hybridoma; infection; immunosuppression; hepatitis;
                                                                                                                                                                      80 adsvkgrftisrdnskntlflqmhslraadtgvyycakdqlyfgsqspghy---wvqgtl 136
                                                                                                                                                                                          1 EVOLLESGGGVVQPGRSLRLSCAASGFTFKTYGMHWVRQAPGKGLEWVAGISFDGSNQYY 60
                                                                                                      20 qvqlvesgggvvqpgrslrlscaasgftfsrygmhwvrqapgkglewvavisydgsnkwy 79
                                                                          3; Gaps
                                          Score 657; DB 19, Length 141;
Fred No 5 57e-43.
                                                                          Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "complementarity determining region 1"
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                                                               Fred No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             W24984 standard; Protein; 141 AA.
                                                                               .,6
                                            Query Match
Best Local Similarity 75.2%.
Matches 94; Conservative
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US-538796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "leader sequence"
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"VhIII region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20..141 "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JUN-1994; US-259372.
variable chain of PE1-1. Sequence 141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-904517.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                liver transplant.
                                                                                                                                                                                                                                                  137 vtvss 141
                                                                                                                                                                                                                                                                                 121 VTVSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-SEP-1986;
31-OCT-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAY-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-SEP-1986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                     Sednence
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A process for isolating and synthesising human monoclonal anti-tumour antibodies has been produced. The process involves: (a) constructing at least one fusion phage library from the peripheral blood lymphocytes (PBLs) of a cancer patient; (b) screening for anti-tumour antibodies in the phage library in a binding assay with cultured 'uncour antibodies in same type as the patient's tumour; (c) removing extraneous antibodies by absorption against normal human cells; (d) cloning the phage selected in steep (b) and (c); (e) assaying the specificity of the cloned phace by incubating the phage with at least two types of cultured normal cells; and (f) further testing the specificity of cloned phage that do not bind to either cell line of cultured normal cells in further that do not bind to cultured tumour cells derived from more than one other tumour that is not the patient's tumour. The present sequence represents a human heavy
chromatography on Q-Sepharose. The heavy and light chains of the Mabs were isolated and their amino acid sequences determined. Primers were generated and used to amplify cDNA synthesised from RNA purified from acach bypridoma cell line. The sequences of the heavy and light chains (nucleic acid and amino acid) from Mabs PEI 1, 2Ml 1, 2Ml-2 and MNS-4 shown in 185838-45 and W24944-91. The Mabs are he used to treat HBV infections in immunosuppressed patients or patients with chronic active hepatifis, especially liver transplant patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigens for studying tumouriquesis or for use as anti-cancer vaccines. The human antibodies have low immunogenicity in humans compared to murine monoclonal antibodies (MAbs). Since the antibodies are isolated from fusion phage libraries, their affinity and specificity for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            not the patient's tumour. The present sequence represents a human heavy chain antibody, from an scrv antibody lusion phage library, produced by a method as described above. The antibodies produced can be used for a method as described above. The antibodies produced can be used for diagnostic and therapeutic applications and for solating tumour parcines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 adsvkgrftisrdnskntlflgmhslraadtgvyycakdqlyfgsgspqhy---wvgqtl 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ADSVKGRFIVSRDNSRDTVFLQMSSLRLEDTAVYYCATEGSPFGS1KGRYYLENWGQGTL 120
                                                                                                                                                                                                                                                                                                                                                       20 qvqlvesgggvvqppgrslrlscaasgftfsrygmhwvrqapqkqlewvavisydqsnkwy ^{79}
                                                                                                                                                                                                                                                                                                                                                                                                   1 EVQLLESGGGVVQPGRSLRLSCAASGFTFKTYGMHWVROAPGKGLEWVAGISFDGSNOYY 60
                                                                                                                                                                                                                                                                                                       9; Mismatches 19; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-melanoma antibody héavy chain clone V86.
Human; monoclonal antitumour antibody; peripheral blood lymphocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prodn. of human monoclonal anti-tumour antibodies - by screening a
fusion phage library produced using peripheral blood lymphorytes
from a cancer patient
                                                                                                                                                                                                                                                  Query Match 71.3%; Score 657; DB 23; Length 141; Best Local Similarity 75.2%; Pred. No. 5.57e-43; Matches 94; Conservative 9; Mismatches 19; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer; tumourigenesis; anticancer vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W13524 standard; protein; 140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-OCT-1997 (first entry)
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(UYYA.) UNIV YALE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 vtvss 141
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23-JAN-1997.
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                                                                                                                                                                             61 ADSVKGRFIVSRDNSRDTVFLQMSSLRLEDTAVYXCATEGSFFGSIKGRYYLENWGGGTL 120
                                                                                                                                                         61 adsvkgrftisrdnskntlylqmnslraedtavyycar-gwglrgeegdyymdvwgkgtm 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human volunteers were interest with hepatitis B vaccine. MD3-4, ZM1-2, ZM1-1 and PE1-1 hybridoma cell lines were derived from lymphocytes of individuals immunised with Heptavax (Merck & CO).

Antibodies PE1-1, ZM1-1, M21-2 and MD3-4, belong to the IgG1 cias.

Antibodies PE1-1, ZM1-1, M21-2 and MD3-4, belong to the IgG1 cias.

The cell lines producing PE1-1, ZM1-1 and ZM1-2 were deposited as AFC FM924, 9191 and 9192 respectively. The cell lines all behave as typical (mouse x human) x human hybridomas and produce their respective Abs in concs. ranging up to 25 mg/l in standard suspension culture. The heavy variable (VH) and light variable (LH) sequenced. Total RNA was extracted from 10(7) hybridoma cells
                                                                                                  1 qvqlvqsqqqlvqpqqslrlscaasqftfssyamswvrqapqkqlewvaaisqsqqstyy 60
                                                                                                                            1 EVQLLESGGGVVQPGPST,PLSCAASGFTFKTYGMHWVPQAPGKGLEWVAGISFDGSNQYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of each cell line. ss DNA was synthesised using AMV-reverse transcriptase and oligo-dT as primer. PCRs were performed and amplified DNA was size selected. ss DNA for sequencing was isolated from each postitive clone after superinfection with MI3K07. Sequencing was by the dideoxy chain termination method (Sanger
                                                                       1; Gaps
                                                                                                                                                                                                                                                                                                                                        Sequence of the VH region of monoclonal antibody PE1-1 against hepatitis B virus surgace antigen. Menatitis B virus; surface antigen; monoclonal antibody; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal antibodies active against Hepatitis B surface antigen - for diagnosis and treatment of Hepatitis B virus Example; Page 35, 53pp; English.
                                            Length 140;
  line can be improved by generic manipulations
                                         Score 653; DB 23; Length 14
Pred. No. 1.186-42;
20; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                    T 13
R54047 standard; Protein, 143 AA.
                                         Query Match
Best Loral Similarity 69 6%;
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                           08-NOV-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69..85
                                                                                                                                                                                                                                                                                                                                                                                   HBSAG; diagnosis; HBV.
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tumear cell line ca
Sequence 140 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label- VH III
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                                                                                                                                                                                                              120 vtvss 124
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70.7%; Score 651; DB 9; Length 143;

Query Match

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80 adsvkgrftisrdnskntlflqmhslraadtgvyycakdqlyfgsqspghy----wvqgtl 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ADSVKGRFIVSPRNSPRTVFLQMSSLRLEDTAVYYCATEGSPFGSIKGRYYLENWGQGTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ADSVEGRETVSFONSROTVFLQMSSLPLEDIAVYYCAFEGSPROSIRGHYYLENWOLGTL 120
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Disclosure, Page 70, 130pp; English.

B-cell superantigen (849) is a fragment of SpA D domain that
specifically binds the Fab portion of variable region restricted
antibodies. The SAG is used to enhance production of VH, sepecially
VH3, restricted Abs. During attempts to identify sAgs, as sequences
(R54784-801) of H chains from Ig reactive with mod-SpA, and as and
FNA sequences (FS4862-15, OA4842-55, Of VH regions of SpA binders
obtained from combinatorial libraries were determined. IgM protein
KIM is derived from the germline configuration of a VH gene
                                                                                                                                                                                                                                                        20 gyglvesgggvygpgrslriscaasgftfsrygmhwyrgapgkglewyavisydgsakwy 79 (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974) (1974
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                                                                                                                                                                                                                                                                                                                                                                                                                                1 EVOLLESGGGVVQPGRSLPLSCAASGFTFKTYGMHWVPQAPGKGLEWVAGISFDGSNQYY 60
                                                                                                 3; Gaps
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SpA-domain D; Ig binding region; IgM. B-cell superantigen, sAg,
superantigen; heavy chain variable region; VH3 restricted antibody;
VH; protein-A; KIM; B-lymphocyte; vaccine.
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Fred No 1,720-42,
10; Mismatches 19; Indels
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R54789 standard; peptide; 125 AA.
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        Rest Loss Similarity 74.2%,
Matches 92; Conservative
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29-OCT-1993; U10555.
30-OCT-1992; US-969936.
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WO9409818-A.
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WO9409818-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                All verman 53.

Well. 94.167127/20.

Well. 94.167127/20.

Stimulating produ. of variable region gene family restricted antibodies - through B-cell super-antigen vaccination bisclosure; Page 71: 130pp; English.

Disclosure; Page 71: 130pp; English.

A B-cell superantigen (849) is a fragment of SpA D domain that specifically binds the Fab portion of variable region restricted specifically binds the Fab portion of variable region restricted application of the specially antibodies. The SAG is used to enhance production of WH, especially WH3, restricted Abs. During attempts to identify sAgs, as sequences (R54784-801) of H chains from I reactive with mod-SpA, and as and sequences (R54784-16, 064842-56) of WH regions of SpA binders obtained from combinatorial libraries were determined. 19M protein RIV is derived from the germline configuration of a VH gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

70.6%; Score 650; DB 9; Length 125;
Best Local Similarity 68.8%; Pred. No. 2.07e-42;
Matches 86; Conservative 20; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: Tue Feb 24 07:10:46 1998 Job time: 35 secs.
                                       (REGC ) UNIV CALIFORNIA.
11-MAY-1994.
29-OCT-1993; U10555.
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 125 AA;
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US-08-844-215-3.rsp

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Pelease 2 ID John F. Collins, Riocomputing Pesearch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07-06-43 1948, MasPar time 5-41 Seconds 501.596 Million cell updates/sec Pun on

Tabular output not generated.

>US-08-844-215-3 (1-128) from USO8844215.pep 915 1 EVQLLEQSGAEVKRPGSSVK......NCYPGFFQOWGQGTLVTVSS 128 Description: Perfect Score:

Sequence:

Scoring table:

PAM 150 Gap 11

59021 seqs, 21210389 residues

Searched:

Post-processing Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot34
lipart1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Mean 40 966: Variance 67 504; scale 0 505 Statistics Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ĮD	Des	Description	lon		Pred. No.
1	553	60.4	117	Ŋ	HV1A_HUMAN	SI	HEAVY	CHAIN	V-I RE	1 -6
7	484	52.9	117	ľ	HV1B_HUMAN	Ľ	HEAVY	CHAIN	PRECITE	4 630-88
3	479	52.3	117	u)	HV1G_HUMAN	T.G	HEAVY	CHAIN	PRECITE	7.400-87
4	7	51.4	143	വ	HV1C_HTMAN	S	HEAVY	CHAIN	PRECUR	120-8
Ŋ	435	47.5	114	2	HV00_MOUSE	10	HEAVY	CHAIN	V REGI	2.890-76
9	431	47 1	125	K.	HULF_HUMAN	E4 (7)	HEAVY	CHAIN	Ed 1-1	620-7
7	428	46.8	140	Ŋ	HV02_MOUSE	ΒÏ	HEAVY	CHAIN	PRECUR	1.37e-74
0 0	426	٠.		r)	HV03_MCUSE	SI	HEAVY	CHAIN	V REGI	
6	434	46.3	124	Ŋ	HV1D_HUMAN	Ω	HEAVY	CHAIN	V-I RE	
10	423		124	'n	HV1E_HUMAN	SI	HEAVY	CHAIN	V-I RE	2.140.73
11	414	45.2	122	Ŋ	HV3G_HUMAN	Si	HEAVY	CHAIN	V-III	3.01e-71
12	402	43.9	117	'n	HV14_MOUSE	IG	HEAVY	CHAIN	рреспр	2 15e-fig
13	400	٠.	117	S	HV13_MOUSE	ij	HEAVY	CHAIN	V REGI	6.43e-68
14	400	43.7	117	2	HV12_MOUSE	IG	HEAVY	CHAIN	V REGI	6 430-68
15	395	43.2	118	S	HV51_MOUSE	ij	HEAVY	CHAIN	V REGI	.87e-6
16	394	43 1	117	ŗ,	HV52_MOTISE	ΙĊ	HEAVY	CHAIN	PPECUR	1.700-66
17	391	42.7	117	u)	HV06_MOUSE	13	HEAVY	CHAIN	PRECUR	.75e-6
	389	42 5	117	r	HV04_MOTISE	13	HEAVY	CHAIN	PPECUP	9-009
19	389	42 5	117	ĸ,	HV05_MOTISE	Ę	HEAVY	CHAIN	PRECUR	2.60e-65
	389	42.5	100	רט	HV50_MOUSE	SH	HEAVY	CHAIN	V REGI	2.60e-65
21	389	42.5	\sim	L)	HV48_MCUSE	S	HEAVY	CHAIN	PPECUR	2.600-65
22	383	42 5	2.20	ď	HA01_MOUSE	S.	HEAVY	CHAIN	PRECUR	2.600 65

117 AA

Eac.

STANDARD

RESULT 2 ID HV1B_HUMAN

.49e- 01e-	286-6 .56e-6	9-0	.19e-5	.51e-5	23e-5	.53e-5	. 596-5 . 966-5	.83e-5 .68e-5	. 926.5	.236-5	.09e-5
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HVIA_BUMAN STANDARD; PRT; 117 AA. 101.42.1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SECTENCE (PEDATE) 21-JUL-1986 (REL. 01, LAST SECTENCE (PEDATE) 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE) 19.40.40.1986 (REL. 01, LAST ANNOTATION UPDATE) 19.40.40.1986 (REL. 01, LAST ANNOTATION UPDATE) 19.40.40.1986 (REL. 01, LAST ANNOTATION UPDATE) 19.40.40.40.10.108.108.108.108.108.108.108.108.108	G0.4%, Score 553; DB 5, Length 117, Best Local Similarity 80 6%, Pred No. 7.614-165, Matches 79, Conservative 10, Mismatches 8, Indels 1, Gaps 1 1 qq1v-qsqaevkkpgssvkvsckasgqtfsrsaliwyrqapqqglowmqqivpmfgppn 59 1 qq1v-qsqaevkkpgssvkvsckasgqtfsrsaliwyrqapqqglowmqqivpmfgppn 59 1 11:
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20 qvqlv-qsgaevkkpgasvkvsckasgytftgyymhwvrqapgqglewmgrinpnsggtn 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IG HEAVY CHAIN PRECURSOR V-I REGION (V35).
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTERRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 88296408.
MATSODA F., LEE K.H., NAKAI S., SATO T., KODAIRA M., ZONG S.Q.ONHO H., FUKUHARA S., HONJO T.:
FMRO J. 7:1047-1051(1988).
                                                                         METAZOA: CHORDATA: VEPTERRATA: TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG HEAVY CHAIN V REGION (V35).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 52.3%; Score 479; DB 5; Length 117;
                                                                                                                                                                                                                                                     IG HEAVY CHAIN V REGION (HG3)
                                                                                                                                                                                                                                                                                                              Length 117;
                                                                                                                                                                                                                                                                                                            Query Match 52.9%; Score 484; DB 5; Length 117; Best Local Similarity 70.7%; Pred. No. 4.63e-88; Matches 70; Conservative 15; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Mismatches 17; Indels
                                                                                                                                          MEDLINE; 83144028.

RECHAVI G., RAM D., GLAZER L., ZAKUT P., GIVOL D.: PROC. NATL. ACAD. SCI. U.S.A. 80:855-859(1983).

EMBL; J00240, G553411; --

PIR: ACA0204, HVHHG.

HSSP; P01810; 1FVB.

    79 yaqkfqgrvtstrdtsistaymelsrlrsddtvvyycar 117

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                                                                                                                                                                                                                                                                                                                                                                                                                                                117 AA; 13009 MW; FAA560D1 CRC32,
                                                                                                                                                                                                                                                                          117 117 117 117 117 AA; 12946 MW; BCC8BIDB CFC32;
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01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
    21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
10 HEAVY CHAIN PRECUPSOR V. 1 FEGION (HG3).
HOMO SAPIENS (HUMAN).
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PIR; S00476; HVHU35.
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                                                                                                 EUTHERIA; PRIMATES.
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HV1G_HUMAN
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SEQUENCE
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                                                                                    EUKARYOTA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 51.4%; Score 470; DB 5; Longth 143; Local Similarity 56.9%; Pred. No. 1.12e-84; es 74; Conservative 23; Mismatches 29; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                KENTEN J.H., MOLGAARD H.V., HOUGHTON M., DERRYSHIRE R.B., VINEY J., BRILL L.O., GOULD H.J.: PROC. NATL. ACAD. SCI. U.S A 79-6661-5665(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BENICH H.H., JOHANSSON S.G O., VON BAHR-LINDSTROM H.; LOPLED BENICH (IN) IMMEDIATE HYPERSENSITIVITY: WODERN CONCEPTS AND DEVELOPMENTS, BACH M.K., ED., PP.1-36, MARCEL DEKKER, NEW YORK, (1978).
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EUKAKYOTA; METAZOA, CHORDATA, VERTEBRATA: TFTPAPONA; MAMMALIA:
EUTHERIA; RODENTIA.
                                                                                                                                                                         HOME SAFIENS (HUMAN)
EUKRAYOTA, METAZOA: CHORDATA; VEKTERRATA; TETKAPODA: MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IG HEAVY CHAIN V REGION (ND).
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                                                             21-JUL-1986 (REL. 01, CREATED)
21-JUL-1985 (REL. 01, LAST SEQUENCE UPDATE)
61-NOV-1999 (PEL. 16. LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PRECURSOR V-I REGION (ND) (FRAGMENTS).
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IH -> HI (IN REF. 2).
VG -> GV (IN REF. 2).
MISSING (IN REF. 2).
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21-JUL-1986 (REL 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL 01, LAST ANNOIATION UPDATE)
1G HEAVY CHAIN V REGION (ANTI-ARSONATE ANTIBODY).
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              143 AA.
                 PRT;
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HVC0_MOUSE STANDARD;
                    STANDARD;
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HSSP; P01607; 1FGV.
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MEDLINE; 79195438.
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121
143
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LT 4
HV1C_HUMAN
P01744;
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                                                                                                                                                                                                                                                                                                                                                 1 evgl-qqsgaelvkagssvkmsckatgytfssyelywvrqapgqgledlg-yissssayp 58
                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVOLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVRQAPGGGLEWMGGSISFFGT-S 59
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EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA; MAMMALIA;
EUTHERIA: PRIMATES.
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47.1%: Score 431, DB 5, Length 125,
Best Local Similarity 49.2%; Pred. No 2.62e-75;
Matches 63; Conservative 26; Mismatches 36; Indels
                                                                                                                                                                                                      Query Match 47.5%; Score 435; DB 5; Length 114 Best Local Similarity 67 0%; Pred No 2 89e-76; Matches 71; Conservative 19, Mismatches 12, Indels
                                                                                                                                                                                                             Length 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 nyaqkfqgrvtitadestntaymelsslrsedtavyfcavrvisry 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMUNOGLOBULIN V PRSTON: ANTIARSONATE ANTIBODY NON_TEP 114 114
                                                                                                      NON_TEP 114 114 SEQUENCE 114 AA; 12555 MW; 1A027F1D CPC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 96 RY SIMILARITY.
125 125
125 AA; 13579 WW; 67450023 CPC32;
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21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-I REGION (MOT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 AA
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BY SIMILARITY.
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KOJIMA M. KOIDE T., ODANI S., ONO T.;
MOL. IMMUNDL. 23:169-174(1986).
PIR; A02025; HVHUMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V SEGMENT
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IMMUNOGLOBULIN V PEGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98
107
125
125
PIR; A02022; G1MSAA.
HSSP; P01772; 1FGV.
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HV02_MOUSE
P01746;
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HV1F_HUMAN
P06326;
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FIRE T INMINOL 12:1923-1032(1982).

-!- FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE. THE AUTHORS CONCLUDE THAT ALL OF THESE TO PEGIONS HAVE PEARANGED TO THE SAME J SEGMENT, JH2.

PIP: ACCORD. HANG.

HSSP; PO1789; 6FAB.

IMMUNGLOBULIN V PEGION, ANTIAPSONATE ANTIBODY; HYBRIDOMA.
                                                                                                                                                                                                                                                                                                                                                                                                                               20 evgl-ggsgaelvragssvkmsckasgytftsyginwykgrpggglewigyinpgngyin 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EVQLLEQSSAEVKKPGSSVKVSCKASGGTFSGHVTSWVPQAPGGGLEWMGGSTSFFGTSN 60
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                                                                                                                                                                                                                                                                                                                                                                                   7; Gaps
STRAIN=A/J;
MEDDINE; 82152818.
MEDDINE; 82152818.
GAPPA T D : And All (1902)
SCIENCE 216 And All (1902)
PERE: JOO493: G195077 - .
PIR: A02028; HVMSG7.
HSSP. POT789; KFAB
IMMUNASLABGEIN V EESION, ANTIARSONATE ANTIBODY, HYBPINOMA, SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUS MUSCULUS (MOUSE).
EUKAPYOTA, METAZOA, CHORNATA, VERTERRATA, TETRAPODA, MAMMALLA;
EUTHERIA, RODENTIA.
                                                                                                                                                                                                                                          IG HEAVY CHAIN V REGION (93G7).
                                                                                                                                                                                                                                                                                                                                   Score 428; DB 5; Length 140; Fred. No. 1.37e-74, 27; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 120;
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46.6%; Score 426; DB 5; Length 120
Best Local Similarity 53.5%; Pred. No. 4.11e-74;
Matches 68; Conservative 29; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE, 83131846.
SIEKEVIIZ M., GEFTER M.L., BPOREUR P., PIRLET P.,
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21-JUL-1986 (REL. 01, LAST SECUENCE UPDATE)
21-JUL-1986 (PFL. 01, LAST SECUENCE UPDATE)
1G HEAVY CHAIN V REGION (36-65).
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                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 54.7%;
Matches 70; Conservative
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NON_TEP
SEQUENCE
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Matches 64; Conservative
                                                                                                                                                                                                                  MEDLINE; 81013859.
LEHMAN D.W., PUTNAM F.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                        IMMUNOGLOBULIN V REGION.
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                                                                                                   STANDARD,
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HSSP; P01789; 11GI.
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117 1
117 AA.
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HSSP; P01607; 2FGW.
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                                     114 qgvlvtvss 122
                                                          120 QGTLVTVSS 128
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P01758;
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SEUCENCE
                                                                                                   HV3G_HUMAN
P01768;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                      60 NSAQKEQGRVSITADESASTAYMELSSLPSEDTALYYCAKDPPPFCSGGNCYPGFFUUWG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l qvqlm-qsgaevkkpgssvrvscktsggtfvdykglwvrqapgkglewvgqiplrfngev 59
                                                                                                                                                                                                                                                                                                     8, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANDREWS D.W., CAPRA J.D.:
BIOCHEMISTRY 20:5822-5830(1981).
-!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLÜBULIN
                                                                                                                                    ANDREWS D.W., CAPRA J.D.;
BIOCHEMISTRY 20:5822-5830(1981).
-i- THIS CHAIN WAS ISOLATED FROM AN 1GM WITH ANTI-GAMMA GLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                           10-10-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
IG HENYY CHAIN V-I REGION (WOL).
HOMO SAPIENS (HUMAN).
EUTHERRAYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

46.2%; Score 423; DB 5, Length 124;
Best Local Similarity 54.3%; Pred. No. 2.14e-73;
Matches 70; Conservative 23; Mismatches 28; Indels
                                                                                                                                                                                                                                                  Score 424; DB 5; Length 124;
Pred. No. 1.24e-73;
20; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PYREGLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                            PYRROLIDONE CARBUXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 AA; 13732 MW; C1E9663D CRC32;
                                                                                                                                                                                                                     124 124
124 AA; 13684 MW; 479BD3BE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REI, 01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 124 AA
              124 AA
              PPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG HEAVY CHAIN V-I REGION (SIE).
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 55.8%;
Matches 72, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR, A02044; M1HUSI.
HSSP; P01857; 2FGW.
IMMUNOGLOBULIN V REGION.
                                                                                                                                                                              PIR; A02043; MIHUWL.
HSSP; P01607; 1FGV.
IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD,
               STANDAFD
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                                                                                                                               MEDLINE; 82046599.
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                HV1D_HUMAN
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NON_TER
SEQUENCE
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SEQUENCE
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                                                                                                                     SEQUENCE.
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      RESULT
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60 gvylkwe-rvtvslkpsfngaymelvnlfneddavyycarew-k--qqvnvnp--ldywq ll3
                         1 qvelve sgggyvzpyrslriscaasgftfsnyamhwyrqppqkqlewva-visybdbbk 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROC. NATL. ACAD. SCI U.S. A. 77.3239-3243(1980).
-- THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A PATIENT WITH MACROSLOBULINEMIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIVOL D., ZAKUT R., EFFRON K., RECHAVI G., RAM D., COHEN J.H.: NATURE 292:426-430(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUS MUSCULUS (MOUSE).
BUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA:
                                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; METAZOA; CHOKDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.2%; Score 414; DB 5; Length 122; 49.5%; Pred No 3.01e-71; varive 30; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYRROLIDONE CARROXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12972 MW, 9410001E 08/325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 122
122 AA, 12558 MW, 4AF2ER10 OPCM2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE HEDATE)
01-JUL-1996 (REL. 34, LAST ANNOTATION UPDATE)
1G HEAVY CHAIN PRECUPSOR V PEGION (108A).
                                                                                                                                                                                                                                                                                                 21-UUL-1986 (REL. 01, CREATED)
21-UUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-UUL-1986 (PEL. 01, LAST ANNOTATION HEPDATE)
11G HEAVY CHAIN V-111 KEGIÓN (CAM).
HOMO SAPLENS (HUMAN).
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BY SIMILARITY

96

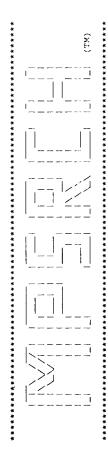
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HSSP; P01772; 1FGV.
IMMUNGSLOBULIN V REGION; GLYCOPROTEIN.
                                                         DISULFID
CARBOHYD
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SET TES
                                                                                                                                                  20 ergl-ggsgpelvkpgasvkisckasgy+f+dynmhwykgshgkslow)gyiypynggtg 79
                                                                                                                                                                                                        1 EVQLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVPQAPGQGLEWMGGSISFFGTSN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 400; DB 5; Length 117;
Pred. No. 6.43e-68;
23; Mismatches 21; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 evql-qqsqpelvkpgasvkmsckasgytftdyymkwvkqshgkslewigdinpnnggts 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVQLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVPQAPGQGLEWMGGSISFFGTSN 60
                                                                                         gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- THE SEQUENCES OF 10 HYPRIDOMA PROTEINS THAT ALSO BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUP IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOWA PROTEIN HAS ALSO BEEN DETERMINED.
-:- THIS PROTEIN BINDS DEXTRAN.
PIR: A0209; WHMS4E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 83075344.
KEHRY M.R., FUHRMAN J.S., SCHILLING J.W., ROGERS J., SIBLEY C.H.,
                                                                                     -:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT: 117 AA.
PU1256:
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V REGION (MOPC 104E).
MUS MUSCUUS (MOUSE).
EUKAPYÇTA: METAZOA: CHOPDATA: VEPTERPATA: TETRAPODA: MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA: CHORDATA: VERTEBRATA; TETRAPODA; MAMMALIA;
                         Score 402; DB 5; Length 117
                                                      Pred. No. 2.15e-69;
23; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SAQKFQGRVSITADESASTAYMELSSLRSEDTAIYYCAKD 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCHILLING J., CLEVINGER R., DAVIE J.M., HOOD L.;
NATURE 283:35-40(1980)
                                                                                                                                                                                                                                                                    79 ynqkfkskatltvdnssstaymelssltsedsavyyear 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 ynqkfkgkatltvdkssstaymqlnsltsedsavyycard 99
                                                                                                                                                                                                                                                                                                 22 96 BY SIMILARITY.
117 117
117 AA; 13024 MW; E7548A05 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (PEL. 01, CPEATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE D AND J SEGMENTS.
--- THIS PROTEIN BINDS DEXTRAN.
PIR; A26242; MMSJ5
HSSP; P01789; 2F03M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 55.0%;
Matches 55; Conservative
                      Query Match
43.9%:
Best Local Similarity 55.5%;
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDAPD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUTHERIA; RODENTIA
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P01757;
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SEQUENCE
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                                                                                                                                                                                                                                   1 EVQLILEQSGAEVKKPGSSVKVSCKASGGIFSGHVISWVPGAPGGGLEWMGGSISFFGTSN 60
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                                                                                                     Query Match
43.7%; Score 400; DB 5; Length 117;
Best Local Similarity 55.0%; Pred No 6 43e-68;
Matches 55; Conservative 23; Mismatches 21; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24; Mismatches 21; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE.
MEDILNE: 84182519.
DILLEPOR F., PROVENS. J., SIEKEVITZ M., BEYPETTHEP K., PAJEWSKY K., EMPO. J. 3:517-523(1984).
PIR; A02040; MHMS38.
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1988 (PEL. 06, CREATED)
01-JAN-1988 (PEL. 06, LAST SEQUENCE UPDATE)
01-JAN-1989 (PEL. 21, LAST ANNOTATION UPDATE)
1G HARN-1992 (PEL. 21, LAST ANNOTATION UPDATE)
1G HANY CHAIN V PERION (AC38 205 12)
MUS MUSCUUS (MOUSE).
EVRAPYOTA, METAZOA; CHOPDATA; VEPTERPATA; TETPAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 395; DB 5; Length 118; Pred. No. 9.87e-67;
                                                                                                                                                                                                                                                                                                                     61 SAQKFQGPVSTTADESASTAYMELSSLPSEDTAIYYCAKD 100
                                                                                                                                                                                                                                                                             60 yngkfkgkatltvdksstaymglnsltsedsavyycard 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 yngkfkgkatltvdksssatymelrsltsedsavyycar 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12934 MW; 2D1DCE77 CRC32;
                                                                1F6GG304 GEG33;
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                                                                12992 XW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cuery Match 43.2%;

Eest Local Similarity 53.5%;

Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P01772; 1FGV.
IMMUNOGLORULIN V REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98
104
118
96
118
                                            117
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22
118
118 1
22
55
117
117 AA;
                                                                                                                                                                                                                                                                                                                                                                              LT 15
HV51_MOUSE
P06330;
                                         NON_TER
SECTENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
NON_TER
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DOMAIN
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Peb 24 07:07:23 1998; MasPar time 8.32 Seconds 468.76P Million cell updates/sec Run on:

Tabular output not generated.

>US-08-844-215-3 (1-128) from USC8844215.pep 915 1 EVQLLEQSGAEVKKPGSSVK. Description: Perfect Score: Sedneuce.

NOYPGFFQQWGQGTLVTVSS 128

PAM 150 Gap 11 Scoring table:

95051 seqs, 30469580 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir53 Database:

Tanni 2:ann2 3:ann3 4:ann4 5:unann1 5:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unann11 16:unann12 17:unenc 18:unrev

Mean 40.399; Variance 101.115; scale 0.400 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	DB	QI	Description	Pred. No.
	969	76.1	125	7	PH0957	Is heavy chain V reg	9.07e-92
C3	641	70.1	128	7	FH0952	Iq heavy chain V req	9.16e-83
m	637	69.8	129	7	A33548	hearry chain V-	4.120-82
4	635	9 .69	127	7	PH0955	Iq heavy chain V req	8.73e-82
Ŋ	633	6.00	126	7	333548	heavy chain V-	1.850-81
9	625	68.3		7	PH0953	q heavy	3.746-80
7	624	68.2	132	7	PH0954	heavy chain V	5.446-80
80	614	67.1		۲.	S46394	heavy chain V	2.32e-78
σ	611	66 A		7	C33548	Iq heavy chain V-1 r	7.136-78
10	611	8.99	627	7	S14683	Iq mu chain precurso	7.13e-78
11	610	66.7		7	PH0962	heavy cha	1.04e-77
12	609	9.99		7	A49590	Iq heavy chain V reg	1.51e-77
13	605	66.1		7	S36261	heavy chain V	6.75e-77
14	603	62.9		^	PH0959	Iq heavy chain V req	1.43e-76
15	601	65.7		۲-	PH0958	Iq heavy chain V red	3.02e-76
16	601	65.7		7	PH0960	heavy chain V	3.02e-76
17	598	65.4		۲٠	PL0105	anti-PR2 erythrocyte	9.396-76
18	594	64.9		7	S26915	Ig heavy chain V reg	4.15e-75
19	594	64.9	116	7	531698	Ig heavy chain precu	4.15e-75
02	594	64.9	119	۲-	PH0961	Ig heavy chain V reg	4.15e-75

4 15e-75	.15e-7	.04e-7	.78e-7	696-7	.546-7	.04c-7	54e-7	.36e-6	27e-6	.84e-6	.61e-6	,15e-6	.15e-6	.71e-6	.23e-6	.36e-6	.06e-6	.02e-5	.52e-6	0.7e-6	.275-6	.6le-6	.57e-6	086-6
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#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross'references MUID:92202880
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#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202889
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1#formal_name Homo sapiens #common_name man
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17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
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Proc. Natl. Acad. Sci. U.S.A. (1989) 86:5913-5917

Developmentally restricted immunoglobulin heavy chain variable region gene expressed at high frequency in lymphocytic leukemia.
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#domain immunoglobulin homology #label IMM\
#region complementarity-determining 1\
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#region framework 2\
#region complementarity-determining 2\
#region framework 3\
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#accession A33548
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#title Evidence for somatic selection of natural automatipodies.
#cross-references MUID:92202880
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#title Developmentally restricted immunoqlobulin heavy chain variable region gene expressed at high frequency in chronic lymphocytic leukemia.
#cross-references MUID:89345575
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J. Exp. Med. (1992) 175:983-991
Evidence for somatic selection of natural autoantibodies
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                                                                      Ig heavy chain V-1 region (AND) - human
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*superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; immunoglobulin
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J. Mol. Piol. (1994) 229:68-78
In vitro assembly of repertoires of antibody chains on the
surface of phage by renaturation.
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#journal J. Exp. Med. (1992) 175.983-991
#title Evidence for somatic selection of natural autoantihodies
#cross-references_MUID:92202880
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Query Match 68.3%; Score 625; DB 7; Length 135; Best Local Similarity 79.5%; Pred. No. 3.74e-80; Matches 89; Conservative 14; Mismatches 5; Indels
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Proc. Natl. Acad. Sci U.S A (1989) 86:5913-5917
Developmentally restricted immunoglobulin heavy chain
variable region gene expressed at high frequency in chronic
lymphocytic leukemia.
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Local Similarity 73 9%; Pred No 7 13e-78;
Les 99; Conservative 12, Mismatches 16, Indels 7, Gaps
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17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
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                                                                                                                                                            #domain immunoglobulin homology #label IMM
th 132 #molecular-weight 14293 #checksum 7515
                                                                                                                                                                                                                                 Match 67.1%; Score 614; DB 7; Length 132; Local Similarity 72.2%; Fred. No. 2.32e-78; es 96; Conservative 17; Mismatches 14; Indels
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#accession C33548
preliminary
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*superfamily immunoglobulin C region; immunoglobulin homology
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           Ig mu chain precursol, membrane bound (clone 201) - human
#formal_name Homo sapiens #common_name man
31-Dec-1991 #sequence_revision 31-Dec-1991 #text_chande
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#journal J. Exp Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#across-references Mulb:9222880
#accession PH0962
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                                                                                                                                          Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. (1990) 18:4278
Complete nuclectide sequence of the membrane form of the
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17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
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Pred. No. 1.04e-77;
12; Mismatches 10; Indels
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12; Mismatches 16; Indels
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#cross-references MUID:90332450
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##cross-references EMBL:X17115
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Best Local Similarity 76.6%;
Matches 98; Conservative
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Local Similarity 73.9%;
Les 99; Conservative
                                                                                                          S14683; S08047
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##note sequence extracted from NCPI backbone
FICATION #superfamily immunoglobulin V region; immunoglobulin homology
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Embleton, M.J.: McCafferty, J : Baier, M.: Holliger, K P ;
Gorick, B.D : Hughes-Jones, N C : Hoogenhoom, H P.: Winter.
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Human anti-self antibodies with high specificity from phage
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1 gvglv-gsgaevkkpgssvkvsckasgdt[ssyaiswvrqapggalewmgdipifgtan 59
                                      1 EVOLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVP@AP@@@lewmaasisFFGTSN 60
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03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
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#title Recombinant human Fab to glycoprotein D neutralizes infectivity and prevents cell to-cell transmission herpes simplex viruses 1 and 2 in vitro.
#cross-references MUID-04105168
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Ig heavy chain V region (clone alpha-TNF-E7) - human
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Pred. No. 1.51e-77;
15; Mismatches 18, Indels
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##residues 1-121 ##label BUR
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Matches 87; Conservative
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# fournal J Exp Mrd. (1942) 175-983-991
# title Evidence for sometic selection of natural autoantibodies.
# creferences MUID:92202880
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Ig heary chain V region (G6' T.226) · human (fragment)
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17-Apr-1993 *sequence_revision 17-Apr-1993 *text_change
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                                                    preliminary; nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                             Score 605; DB 7; Length 116; Pred. No. 6.76e-77;
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#region framework 2\
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                                                                                                                                                                                                                                                                                            #length 116
                                                                                   ##molecule_type mRNA
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## 1-122 ##label MAR #superfamily immunoqlobulin homology heterotetramer; immunoqlobulin
                 #authors Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J. B. Bridneral J. Exp. Med. (1942) 175;983-991 Evidence for somatic selection of natural autoantibodies. #title #cross-references MUID:92202880
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 65.7%; Score 601; DB 7; Length 122; Best Local Similarity 82.9%; Fred. No. 3.02e.76; Matches 87; Conservative 10; Mismatches 6; Indels 2; Gaps
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*domain immunoglobulin homology *label IMM\
*region complementarity-determining 1\
*region framework 2\
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##molecule_type DNA
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KEYWORDS he
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SUMMARY
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Pelease 2.15 John F. Collins, Biocomputing Research Unit. Copyright (c) 1994, 1994, 1995 University of Edinburgh, W.K Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07-35-05 1998; MasPar time 3 29 Seconds 198.618 Million cell updates/sec Pun on:

Tabular output not generated.

Title: Description: Perfect Score:

>US-08-844-215-3 (1-128) from US08844215.pep 915 1 EVQLLEQSGAEVKKPGSSVK......NCYPGFFQQWGQGTLVTVSS 128 Sednence:

PAM 150 Gap 11 Scoring table:

56402 segs, 5095871 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued libackl 2:51 3 52 4 53 5 54 6 55 7:56 8 PCT90 9-PCT91 10-PCT92 11-PCT93 12:PCT94 13-PCT95 14-PCT94

Mean 28.046; Variance 135.560; scale 0.207 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

NO.	Score	Match	Match Length	DB	ID	Description	Pred No.
- -	628	68.6	1 61	133	PCT-US95-0	Sequence 45, Applicati	3.50c-44
7	60B	₩ ₩	120	Π	PCT-11593-1	13	1 930-42
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10	553	60 4	117	۲-	- 474 - OB - 474 -	15	H
11	553	60.4	117	9	US-08-477-	4	1.08e-37
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	553	60.4	117	9	US-08-477-	72	ď
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15	553	60.4	117	Ç,	- 189-L0-SD	4 , A	H
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18	553	60.4	117	9	US-08-477-	10	1.080-37
19	553	60.4	117	7	US-08-481-	15, A	1.080-37
20	553	60.4	117	7	US-08-487-	72,	1.08e-37
21	553	60.4	117	7	US-08-474.	104,	1.080-37
77	553	50.4	117	۲٠	US-08-474-	Sequence 72, Applicati	1.080-37

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CORRESPONDENCE ADDRESS:	JE ADDRESS:		
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	San Francisco		
STATE: Cal	California		
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MEDIUM TYPE.	E. Floppy disk		
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SOFTWARE	Patentin Release	Ć ‡‡	Version #1 25
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STRUCTURE TAR	ARFELTANTED NUMBER: FULLOUSO/OFFE	530/01513	
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PRIOR APPLICA	APPLICATION DATA:		
APPLICATION NUMBER.		TE OB/184,269	
FILING DATE:	25-JAN		
ATTOPNEY/AGENT	_		
NAME: Smith,	, William		
PECISTRATION	11		
REFERENCE/1	REFERENCE/DOCKET NUMBER:	15270-14	
TELECOMMUNICA	TELECOMMUNICATION INFORMATION.	Z	
TELEPHONE	TELEPHONE: 415-543-9600		
TELEFAX: 4			
INFORMATION FOR SEQ ID NO:	R SEG ID NO: 45		

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METHOD FOR STIMULATING PRODUCTION OF VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG
                                                                                                                                                                                                          60 NYAQKEQGRVIITADISISTAYMELSSLRSEDIAVYYCARAPG-YGSGGGCYRGDYXFDY 118
                                                                                                                                                                                                                                     60 NSAQKFQGRVSITADESASTAYMELSSLRSEDTAIYYCAKDPPRFCSGGNCYPG-F-FQQ 117
                                                                                                                                                    1 QVQLV-QSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMGWINPYGNGDT 59
                                                                                                                                                                            1 EVQLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVRQAPGQGLEWMGGSISF-FGTS 59
                                                                                                                        5; Gaps
                                                                                         Score 628, DB 13, Longth 129;
Pred. No. 3 60e-44;
15; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-TVS/MS-PVS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 180 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application PC/TUS9310555 GENERAL INFORMATION:
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                                      TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 129 AA; 13930 MW; 96169 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: FD-21
TELECOMMUNICATION INFORMATION:
TELEFAN: (619) 455-5100
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Howells, Stacy L. REGISTRATION NUMBER 34,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SILVERMAN, GREGG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: THEREOF NUMBER OF SEQUENCES: 51 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-OCT-1993
                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JENGTH: 120 amino acids TYPE: amino acid
LENGIH: 129 amino acids
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                                                                                                             Best Local Similarity 72.5%;
Matches 95; Conservative
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               amino acid
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                          STRANDEDNESS:
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Sequence 12, Application PC/TUS9310555
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIHODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG
                                                                                                                                                                          60 AQKEQGKVIITADESINTAYMELRSLRSDDTAMYYCAKEG--Y---GD-YGRPFDFWGQG 113
                                                                                                                                                                                        15, Mismatches 11; Indels 7; Gaps
                                                                                                                           1 VHLV-QSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGQANY 59
                                                                                                                                          Score 608; DB 11; Length 120;
Pred. No. 1.93e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentln Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
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29-0CT-1993
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MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application PC/TUS9310555.
                                   NAME/KEY: Peptide
LOCATION: 1..120
NCE 120 AA; 13008 MW; 78865 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Howells, Stacy L. REGISTRATION NUMBER: 34,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                     STANDARD;
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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COPPESPONDENCE ADDRESS:
                                                                                / Match 66.4%;
Local Similarity 74.0%;
nes 94; Conservative
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California
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IMMEDIATE SOURCE:
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PCT-US93-10555-12
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                                              LOCATION:
SEQUENCE 120 A
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             CLONE:
                        FEATURE:
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                                                              Score 606; DR 11; Length 120;
Prod No 2:846-42;
15; Mismatches 10; Indels 7; Gaps
                                                                                                      1 VQLV-QSGAEVKKPGSSVKVTCKASGDTFSSSAISWVPQAPGQGLFWMGGIIPIFGTPNY 59
                                                                                                                         2 VQLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVRQAPGQGLEWMGGSISFFGTSNS 61
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No. 1 875-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARD: PATEMITE Release #1 0, Version #1 25
CURRENT APPLICATION DATA.
APPLICATION NUMBER: US/08/217,918
                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION HARBAPLICANT LAKE, PHILIP APPLICANT CARE SPEEG, LARS TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS COPRESPONDENCE ADDRESS.
                                                                                                                                                                                                                                         147 AA
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CLASSIFICATION: 530
TORNEY ARENT
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JENCE 147 AA; 15801 MW; 123306 CN;
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Pred No 1
                          NAME/KEY: Peptide
LOCATION: 1..120
ICE 120 AA; 12984 MW; 80846 CN;
                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/U8217918
Patent No. 5506132
                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08217918
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oirEET 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORREY/AGENT INFORMATION NAME: Smith, Willaim M PROSERFATION NUMBER 30, 223 TELECOMMUNICATION INFORMATION TELEPHONE: (415) 325-2400
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TELEFAX: (415) 326-2422
INFOPMATION FOR SEG IN NO. 4 · SEQUENCE CHARACTERISTICS ·
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                                                               Query Match 66 2%;
Best Local Similarity 74 4%;
Matches 95; Conservative
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IMMEDIATE SOURCE:
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         CLONE:
FEATURE:
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                                               SEQUENCE
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Local Similarity

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                                                                          1 EVQLLEQSSABVKKPGSSVKVSCKASGJESGHVISWVKQAPGQEEWMGGSISFFGISN 60
                                            20 OVOLV-OSGAEVKKPGSSVKVSCKASGGIFSNFAISWVFQAFGQGLEWMGFIMPLFVIST 78
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  92; Conservative 15; Mismatches 18; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 75
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                                                                                                                                                                                                                                                                                                                                                            102 AA.
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SEQUENCE 102 AA; 10940 MW; 55781 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   William M. Smith
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TELECOMMUNICATION INFORMATION:
TELEPHONE. 415-543-9600
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NAME: Smith, William M.
PEGISTPATION NUMBER: 87654
                                                                                                                                                                                                                                                                                                                                                         STANDARD,
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MEDIUM TYPE: Floppy disk
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: California
RY: USA
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                         137 WGQGTTVTVSS 147
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PCT-US92-06185-55
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APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 560; DB 7; Length 102; Pred. No. 2.68e-38; 11; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                       E: Townsend and Townsend Khourie and Crew One Market Plaza, Steuart Tower, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                        102 AA
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  61 SAQKFQGRVSITADESASTAYMELSSLRSEDTAIYYCAK 99
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APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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                                                          PRT:
                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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JENCE 102 AA; 10940 MW; 55781 CN;
                                                                                                                                                                   Sequence 63, Application US/08053131 Patent No. 5661016 GENERAL INFORMATION:
                                                                                                                                        Sequence 63, Application US/08053131.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
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ATTORNEY/AGENT INFORMATION:
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                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Smith, William M. REGISTRATION NUMBER: 30
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Best Local Similarity 80.8%;
Matches 80; Conservative
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California
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5 QVQLV-QSGAEVKKPGSSVKVSCKASGGTFSSYATSWVRQAPGQGLEWMGRIIPILGIAN 63
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                                                                                                                                                                                                  APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TILLE OF INVENTION: Transgenic Non-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                       ADDRESSEE: William M. Smith
STREET ONE Market Plana, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Release #1.0, Version #1.25
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  PRT;
                                                                                                                                                        Sequence 63, Application PC/TUS9210983 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 55, Application US/U7834539A
Patent No. 5633425
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
                                                                                                                    Sequence 63, Application PC/TUS9210983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
JENCE 102 AA; 10940 MW; 55781 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 55, Application HS/07834539A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 63:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 102 amino acids
                                                                                                                                                                                                                                                                               152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                    STREET ONE MALL.
CITY: San Francisco
CTATE: California
                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER PEADARLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-834-539A-55
PCT-US92-10983-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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                                                                                  01-JAN-1900
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COMPULER READABLE FORM:
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  COMPITER
                                                                                                                                                                                TOPOLOGY.
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                                                                                                                                                                                                             CLONE:
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TITLE OF INVENTION: Transgenio No. 553425-Human Animals Capable of
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SECHENIES: 73
                                                                                                                                                                                                                                                                                                                                                                                  5 QVQLV-QSGAEVKKPGSSVKVSCKASGGTFSSYAISWVPQAPGQGLEWMGPIIPILGIAN 53
                                                                                                                                                                                                                                                                                                                                                                                                    1 EVQLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVRQAPGQGLEWMGGSISFFGTSN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application PC/TUS9500067
GENERAL INFORMATION:
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
TILLE OF INVENTION: HUMAN MONOCLONAL ANTIRODIES TO HEPPES
TITLE OF INVENTION: SIMPLEX VIPUS AND METHODS THEPFEOR
NUMBER OF SEQUENCES: 25
                                           ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                               F. Indels
                                                                                                                                                                                                                                                                                                                                              Length 102,
                                                                                                  COMPUTE FEATURE FURM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: PATENTIN FOLOSE #1.0, Version #1.25
CURPENT APPLICATION DATA:
RPLING DATE: 19920205
FILING DATE: 19920205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Spensley Horn Jubas & Lubitz
1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                        64 YAQKFQGRVTITADKSTSTAYMELSSLPSEDTAVYYCAP 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SAOKFOGRVSITADESASTAYMELSSLRSEDTAIYYGAK 99
                                                                                                                                                                                                                                                                                                                                            Score 560, DB 7,
Pred No 2,68e-38,
                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                     14643-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPT:
                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
ENCE 102 AA: 10940 MW; 55781 CN;
                                                                                                                                                                                                                                                                                                                                                      Pred No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application PC/TUS9500067
                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER 14
TELECHMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEPAX: 415-543-5043
                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                            : 102 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                single
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MEDIUM TYPE: Floppy
                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RD 88.
Matches 80: Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                               CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
                             NUMBER OF SECUENCES.
                                                                                                                                                                                                                                                                                                         linear
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                                                                                    USA
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                                                                                   COUNTRY:
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61 FQDRLTITAEVSTSTAYMQLSGLTYEDTAMYYCAR-VA-YMLEPTVTAGGLDVWGQGTTV 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 13; Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: QUEEN, Cary L.
APPLICANT: CO. Man Sung
APPLICANT: CO. Man Sung
APPLICANT: SCHEIDER, William P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK: IMPPOVED HYMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Townsend and Townsend Khourie and Crew
                     OPERATING SYSTEM: PT-100S/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.9%; Pred. No. 5.93e-38;
Matches 83; Conservative 70; Miscatches 19;
                                                                                        F21/1895/000067
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                                                                                                                                                                                                                           FD-3229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Peptide
LOCATION: 1..122
VCE 122 AA, 12999 XW, 86643 CN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application HS/08474040
Patent No. 5693761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15, Application US/08474040.
                                                                                                                                                                                                                                           LELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
TNPORMATION FOR SEQ. TO NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino.
                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
MARE: Halle, Pb D, Lisa A.
PRESISTRATION NUMBER: 38,347
IBM PC compatible
                                                                                                                                                                                                                 PREERBUCE/DOCKET WINEER: FD TELECOMMUNICATION INFORMATION TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               379 Lytton Avenue
                                                                                                      04-JAN-1995
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                                                                CUPPENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE IYPE: peptide IMMEDIATE SOURCE:
                                                                                   APPLICATION NUMBER:
FILING DATE: 04-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.48;
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nes 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Protein
            Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS
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                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                 COUNTRY:
                    STATE:
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SCCXEXEX
     1 QVQLV-QSGAEVKKPGSSVKVSCKASGGTFSRSALIWVRQAPGQGLEWMGGIVFMFGPFN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVQLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVRQAPGQGLEWMGGSISFFGTSN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: /note= "Eu heavy chain amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
ARPLICANT: SELICK, Harold E.
TILE OF INVENTION: HIMPOVED HIMANIZED IMMINOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                  553; DB 7, Length 117
No. 1.08e-37;
     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Townsend and Townsend and Crew LLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 YAQKEQGRVTITADESTNTAYMELSSLRSEDTAFYFCA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SAQKFQGRVSITADESASTAYMELSSLRSEDTAIYYCA 98
                                                                                                                                                                                                                 30,223
ER: 11823-002600
                                                                           CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATE: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: SMITH, Milliam M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-0026(
TELEPHONE: (415) 326-2402
INFORMATION FOR SEQ 1D NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH 117 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Mismatches
                                                     APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 553;
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CE 117 AA; 12472 MW; 77871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08477728 Patent No. 5585089
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                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO FEATURE.
                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 80.6%;
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                 FILING DATE: 07 CLASSIFICATION:
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US-08-477-728-4
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1 QVQLV-QSGABVKKPGSSVKVSCKASGGTFSRSAIIWVRQAPGQGLEWMGGIVPMFGPPN 59
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OTHER INFORMATION: Fu antibody heavy chain."
NCE 117 AA; 12472 MW; 77871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 117;
                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA.
APPLICATION NUMBER: US/08/477,728
FILING DATE: US-07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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Pred, No. 1.08e-37;
10; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11823-002600
                                                                                                                                                                                                                                                                                         FILING DATE: 28'SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13 FEB-1989
PRIOR APPLICATION UMBER: US U7/290,975
FILING DATE: 28'DEC-1988
FILING DATE: 18'ORATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                         115 07/590,274
                                                                  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/08477728 Patent No. 5585089 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/08477728.
COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER. 118
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (415) 326-2400
                                                                                                                                                                                                                         FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IS 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 326-2422 INFORMATION FOR SEC ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Smith, William M
REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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PRT;
                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-FOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
JENCE 117 AA; 12472 MW; 77871 CN;
                                         Seguence 72, Application US/08477728
Patent No. 5585089
                     Sequence 72, Application US/08477728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                               GENERAL INFORMATION:
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US-07-634-278-15
                                                                                                                                                                                    COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CENGIH:
01-JAN-1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XXXXXX
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  1 QVQLV-QSGAEVKKPGSSVKVSCKASGGTFSPSAIIWVPQAPGQGLEWMGGIVPMFGPPN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLLEQSGAEVKKPGSSVKVSTKASGGTFSGHVISWVRQAPGGGLEWMGGSISFFGTSN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1 117
OTHER INFORMATION: /note= "Eu heavy chain amine acid
OTHER INFORMATION: sequence "
NCE 117 AA: 12472 MW: 77871 CN:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, William P.
TILLE OF INVENTION: IMPROVED HUMANIZED IMMUNGLOBLINS
UNDER OF SEQUENCES: 113
COPPESPONDENCE ADDPESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 553; DB 6; Length 117;
Pred. No. 1.08e-37;
10; Mismatches 8; Indels
                                                                                                                            COMPUTER PEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: PatentIn Pelease #1 0, Version #1.25
                                                               E: Townsend and Townsend and Grew LLP
Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 AA
                                                                                                                                                                                                                                                                               APPLICATION NUMBER 155 0/7530,774
FILING DATE: 28 SEP-1990
PPIOR APPLICATION DATA:
APPLICATION NUMBER 157 0/7310,252
FILING DATE: 13-FEB-1989
PPIOR APPLICATION NATA-
APPLICATION NUMBER 16 0/7290,975
FILING DATE: 28-DEC-1988
ATORNEY/AGENT INFORMATION NAME: Smith, William M
PROJESPRATION NUMBER 10,223
PREFERENCE/DOCKET NUMBER 11923-002500
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEPRONE (415) 326-2422
INFORMATION FOR SEQ ID NO: 15-SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 YAQKFQGPVIITADESTNTAYMELSSLRSEDTAFYFCA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SAQKFQGRVSITADESASTAYMELSSLRSEDTAIYYCA 98
                                                                                                                                                                                 CURRENT APPLICATION DATA.
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-7010-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US/05/4,278
FILING PATE: 19-05-1990
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 07/590,274
APPLICATION NUMBER: US 07/590,274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
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                                                                  Abbr...
STREET: TWC can...
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 80.6% nes 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 13
US-08-477-728-72
                                                                ADDPESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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1 QVQLV-QSGAEVKKPGSSVKVSCKASGGIFSPSAIIWVPQAPGGGLEWMGGIVPMFGPPN 59
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APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, William P.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOBLOBLINS
TOTHE OF SCHUENCE: 113
COPPESSONNENCE ADDPESS:
ADDRESSED: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 60.4%: Score 553: UB 6: Length 117; Best Local Similarity 80.6%; Pred. No. 1.08e-37; Matches 79; Conservative 10; Mismatches 8: Indels
                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Pelease #1 0. Version #1.25 CURPENT APPLICATION DATA - 05/08/477,728 FILING DATE: 07-JUN-1905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 AA
                                                                                                                                                                                            STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 YAQKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11823-002600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 97/319,252
PILOR DATE: 13-FFF-189
APPLICATION DATA: 189
APPLICATION DATA: 97/290,975
APPLICATION NUMBER: US 97/290,975
FILING DATE: 28-DEC-198
ATOPNEY AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 11923-00260
TELEPHONE: (415,326-2400
TELEPHONE: (415,326-2420
INFORMATION FOR SEQ. 110 NO: 72: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 28-SEP-1940
PRIOR APPLICATION DATA
APPLICATION DATA
FILING DATE: 15 97/310 nen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER: US/08/477,728
07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
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61 SAQKFQGRVSITADESASTAYMELSSLRSEDTAIYYCA 98
                                                                  . 1 EVQLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVRQAPGGGLEWMGGSISFFGTSN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLV-QSGAEVKKPGSSVKVSCKASGGTFSPSATTWVPQAPGQGLEWMGGIVPMFGPPN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: /note= "Eu heavy chain amino acid
OTHER INFORMATION: sequence."
WCE 117 AA; 12472 MW; 77871 CN;
                                                                                                                                                                       APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
COPPERSPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 117;
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                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/634,278 FILING DATE: 19-DEC-1990 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 60.4%; Score 553; DB 6; I
Best Local Similarity 80.6%; Pred. No. 1.08e-37;
Matches 79; Conservative 10; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.) YAOKFOGRVTITADESTNIAYMELSSLRSEDTAFYFCA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 11823-002600 TELECOMMUNICATION INFORMATION. TELEPHONE. (415) 326-2400 TELEPHONE. (415) 326-2420 INFORMATION FOR SEQ ID NO. 15. SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 03 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY AGENT INFORMATION:
NAME: Smith, William M
PECISTPATION NUMBER
30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                    Sequence 15, Application US/07634278 Patent No. 5530101 GENERAL INFORMATION:
                                                                                                                         CO, Man Sung
SCHNEIDER, William P.
LANDOLFI, Nicholas F.
COELINGH, Kathleen L.
                                           Sequence 15, Application US/07634278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 amino acids
                                                                                                              QUEEN, Cary L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Protein LOCATION: 1..117
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APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                       COUNTRY:
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                   01-JAN-1900
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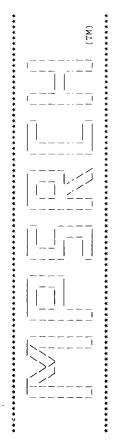
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Gaps
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                                                                                                                                                                                                                                APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: CORLINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNGGIOBLINS
NUMBER OF SEQUENCES. 113
COPPERSONDENCE ANDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.4%; Score 553; DB 6; Length 117; 80.6%; Pred. No. 1.08e-37; atlive 10; Mismatches B; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/h34,278 FILING DATE: 19-DEC-1990 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Smith, William M
FEGISTARION UNBEE: 30,223
REFERENCE/POCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IS 07/290,975
FILING DATE: 28-DE-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READARLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 AA; 12472 MW; 77871 CN:
                 PRT;
                                                                                                                                                                            Sequence 4, Application US/07634278 Patent No. 5530101 GENERAL INFORMATION:
                                                                                                                                        Sequence 4, Application US/07634278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    379 Lytton Avenue
                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO FRATIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 28-SEP-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
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Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Palo Alto
: California
XY: US
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JT 15
US-07-634-278-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                     01-JAN-1900
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Search completed: Tue Feb 24 07:35:16 1998 Job time: 11 secs.

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US-08-844-215-3.rag



Release 2 1D John F. Collins, Riocomputing Pesasch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_FP

Tue Feb 24 07:08:10 1998; MasPar time 7.03 Seconds 252.969 Million cell updates/sec Run on:

>US-08-844-215-3 (1-128) from US08844215.pop 915 Title:

Tabular output not generated.

NCYPGFFQQWGQGTLVIVSS 128 1 EVQLLEQSGAEVKKPGSSVK... Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

111726 segs, 19889129 residues Searched.

Listing first 45 summaries Minimum Match 08 Post-processing:

a-geneseq30 Database:

lipart1 2:part2 3.part3 4.part4 5.part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part12 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23

Mean 30 241; Variance 147 709; scale 0 205 Statistics.

Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

4442 Sequence of antibody 4794 Antibody B888 CEA-specific antibody 779887 CEA-specific antibody 779887 CEA-specific antibody 779887 CEA-specific antibody 7998 CEA-specific antibody 1998 CEA-specific antibody 19	Result No.	Score	Query Match	Length	r r	ID	Description	Pred. No.
2 608 66 4 120 9 R54796 Spå-reactive IgM heav 4 608 65.4 476 6 R31023 Antibody D heavy chai 4 601 65.4 476 9 R12023 Antibody D heavy chai 4 601 64.9 9 R12 R72068 DP10 VH region. Though T 592 64.8 123.23 W19889 CEA-specific antibody D 588 64.3 123.23 W19889 CEA-specific antibody D 588 63.2 120.3 W1988 CEA-specific antibody D 588 65.2 117 4 R2358 Protein encoded by the S 580 60.2 117 2 W1999 CEA-specific antibody D 588 65.3 CC.2 117 2 R399 CEA-SPECIFIC Encoded D 588 65.3 CC.2 124 9 R26914 Human antibody D 588 65.3 CC.2 124 9 R26914 Human antibody D 588 65.3 CC.2 124 9 R26914 Human antibody D 588 65.3 CC.2 124 9 R26914 Human antibody D 588 65.3 CC.2 124 9 R26914 Human antibody D 588 658 659 659 659 659 659 659 659 659 659 659	-	756		481	2	R24442	•	9.75e-54
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61 SAQKFOGRVSITADESASTAYMELSSLRSEDTAIYYCAKDPPRFCSGGNCYPGFFQWGQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A B-cell superattigen (349) is a fragment of SpA D domain that specifically binds the Fab portion of variable region restricted antibodies. The SAG is used to enhance production of VH, especially VH3, restricted Abs. During attempts to identify sAgs, as sequences (R54784-801) of H chains from Ig reactive with mod 'SpA, and as and DNA sequences (R54802-16, Q64812-56) of VH regions of SpA binders obtained from combinatorial libraries were determined. IGM protein KAS is derived from the germline configuration of a VH gene
                                                                                                                                                                                                                                                                                                                                                                   84 yaqkfqgrvtitadeststaymelsslrsedtavyycardngaycsggscysqwfdpwgq 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           additional N-linked glycosylation sites are introduced at locations which impair complement fixing and Fc receptor binding ability. They are preferably located in the CH2 region of the Iq molecule. Antibodies bearing multiple sialyl-Lex determinants are useful for disrupting undesirable interactions between cells or proteins. Disrupting this interaction has therapeutic applications, for example, in minimising inflammation following tissue injury. Sequence 481 AA:
                                                                                                                                                                                                                                                                                                                    1 EVQLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVRQAPGQGLEWMGGSISFFGTSN 60
                                                                                                                                                                                                                                                                                25 qvqlv-qsgaevkkpgssvkvsckasggtfssyaiswvrqapggglewmggiipifgtan 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SpA-reactive igM heavy chain clone RAS.
SpA domain D; Iq binding region; IqM; B-cell superantigen; SAG,
superantigen; heavy chain variable region; VH3 restricted antibody;
VH; protein-A; KAS; B-lymphocyte; vaccine.
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Stimulating prodn. of variable region gene family restricted
antibodies - through B-cell super-antigen vaccination
bisclosure; Page 78: 130pp; English.
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                                                                                                                                                                                             Score 756; DB 5; Length 481;
Pred. No. 9.75e-54;
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                                                                                                                                                                                                                                          14; Mismatches
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R54796 standard; peptide; 120 AA.
                                                                                                                                                                                               Match 82.6%;
Local Similarity 81.3%;
les 104; Conservative
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30-CCT-1992; US-969936.
(REGC ) UNIV CALIFORNIA.
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Disclosure: Fig 2; 35pp; English.

The sequences qiven in R31023-24 represent the heavy and light chains the sequences qiven in R31023-24 represent the heavy and light chains which was derived from peripheral blood lymphocytes from a hepatitis A virus (HAV) sero positive patient. Antibody D is closely related in nature to murine antibody B5B3. Total RNA was isolated from antibody D expressing cells and polyademylated RNA was extracted. These polyARNA's were used to prepare a cDNA library which was screened for human Further heavy (H) chains and two positive clones were detected.

Further heavy (H) chain clones were also isolated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 ysqnfqgrvtitadkststahmeltslrsedtavyycatdryrqanfdrarvqwldpwqq l^{148}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EVQILEQSGARVKYPGSSVYVSCYKASGGTFSCHVISWVRGAPGGGLFWMGGSISFFGTSN 60
                                                        Heavy, light, chain, antibody: D: moncolonal peripheral blood: lymphoryte; hepatitis A virus; HAV; sero; positive; patient; murine: B5B3; polyadenylated; cDNA library; human; kappa; L; H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prodn. of recombinant primate antibodies - useful for treating
infections caused by hepatitis A, B and C, herpes,
cytomegalovirus, AIDS, ARC, also treat multiple sclerosis.
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70.3%; Pred. No. 4.58e-41;
ative 15; Mismatches 22,
                                                                                                                     Location/Qualifiers
        R31023 standard; Protein; 476 AA.
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                                      (first entry)
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                                                                                                                                                                                                                                                                                                       114..121
                                                                                                                                                  "Signal peptide"
                                                                                                                                                                                                                                                                              85..113
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15-JUL-1991; GB-015284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1991; GB-016594.
                                                  Antibody D heavy chain.
                                                                                                                                                               20..49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB-006284
                                                                                                                                                                                                                                                 69..84
                                                                                                                                                                                            50..54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Crowe JS, Lewis AP; WPI; 93-019951/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 qtlvtvss 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; Q35099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arthritis etc
                                                                                                                                                                                                                                                                                                                                                                                                        label= HINGE
                                                                                                                                                                                                                                                                CDR2
                                                                                                                                                                                                                                                                                                                      CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-1992;
                                                                                                                                                                                                         'label = CDR1
                                                                                                                                                                                                                                                                                          FR3
                                     19-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                            label= CH1
                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= CH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP-523949-A
                                                                                                                                                                                                                                    'label= FR2
                                                                                                                                                                                                                                                                                                                                                  FR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                              'label= CH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JAN-1993
                                                                                                                                                                              /label= FR1
                                                                                                           Synthetic.
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This polypeptide sequence comprises the heavy chain variable region (YR), HBBL, obtained by mutagenesis of the YH CDB3 of human carcinoembryonic antigen (hCBA) specific antibody CEA6 (see W19881). A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 -8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 cextracellular domain of hCEA and/or to cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include pairings of YH and VL variants (see W19886-95) obtained by a swell as CEA6 VH and VL variants (see W19886-95) obtained by comparenesis or chain shuffling. An example of a claimed pairing is HBB11 VH with CEA6 VL. (A) is used to detect cells expressing CEA6. In vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 yaqkfqgrltitadeststaymelsslrsedtavyycarhnhny--elyyy--ymdvwqq 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SAQKEQGPVSITADESASIAYMELSSLRSEDTATYYCAKUPPRFCSGGNCYPGFFQQWGQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 gvglv-gsgaevkkpgssvkvsckasgqtfsnspinwlrgapggglewmgsiipsfgtan 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLLEQSGAEVKKPGSSVKVSCKASGGIFSGHVISWVK,APG, 3 LEWMGESISFFGISN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Specific binding members for human cardinosmbiyonic antigen · bind to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells, used for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'n
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Pred. No. 1.81e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                    tumour marker; lung cancer; breast cancer; colon cancer;
                                                                                                                                                                                                                          CEA-specific antibody CEÁS VH mutant HBB11 sequence.
Carcinoembryonic antigen; CEA; human; antibody; scFv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhote "complementarity determining region 1"
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "complementarity determining region 2" Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Osbourn JK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                        W19888 standard; Protein; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match
Local Similarity 71.1%;
Local Similarity 71.1%;
Local Similarity 71.1%;
                                                                                                                                                                                            07-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                               adenocarcinoma; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-00T-1996; GB-021295
07-DEC-1995; GB-025004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAY-1996; GB-010824
                                                                                                                                                                                                                                                                                                                                             Chimeric Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-DEC-1996. G03043
                                                                                                                                                                                                                                                                                                                                                                         Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97-319779/29.
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               121 GTLVTVSS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GTLVTVSS 128
W09720932-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
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                                                                                                                                                                                                                             NAME ON CONTRACTOR OF THE PROPERTY OF THE PROP
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RESULT

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1 grglv-gsgaevkkpgssvkvsckasggtfssyaiswyrgapggglewmggilpifgtan 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soure 594, (48-12, tength 98;
Pred. No. 7.13e-40;
10; Mismatches 4; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L-and H-chain DNA was amplified by PCR from Graves' orbital tissue and clones encoding autoimmune-associated immunoglobulin tissue and clones encoding autoimmune-associated immunoglobulin fragments were obtained a 13/15 clones of H chain (1961) genes showed homology to the closest germline genes, PPIO (200327) and hv1163 (209328) The DNA (200429) and corresp amino acid (PPI) 2) are provided.

PPID 17 are provided.

Sequence 98 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Graves' ophthalmopathy-associated monoclonal antibody - produced by molecular cloning of immunoglobulin genes by PCR Disclosure; Page 68: 94pp; English.
                                                                          Graves ophthalmopathy associated immunoglobulin protein; orbital antigen; monoclonal antibody; heavy chain; H chain; variable region; autoimmunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CEA-specific antibody CEÁ6 VH mutant HRA11 sequence.
Carcinoembryonic antigen; CEA; human; antibody; scFv;
tumour marker; lung cancer; breast cancer; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 yaqkfqgrvtitadeststaymelsslrsedtavyycar 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "complementarity determining region 1" Pegion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CAMB-) CAMBRIDGE ANTIBODY IECHNOLOGY.
                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                             22-SEF-1993; US-124469.
(NICH) NUTHORICE INST DIAGNOSTICS.
MClachlan SM, Rapoport B;
WPI; 95-139383/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W19887 standard; Protein; 123 AA.
R72068 standard; Protein; 98 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euery Match
Best Local Similarity 84.8%;
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-DEC-1997 (first entry)
                                     26-SEP-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adenocarcinoma; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-DEC-1996, G03043.
11-901-1996, SB-211295.
07-DEC-1995, GB-025004.
23-MAY-1996, GB-010824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.35
                                                                                                                                                                                 31..35
                                                                                                                                                                                                                             50..66
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Chimeric synthetic.
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WO9508336-A.
30-MAR-1995.
22-SEP-1994; U10756.
                                                           DP10 VH region.
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                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-JUN-1997.
                                                                                                                                                                                                         /label= CDR1
                                                                                                                                                                                                                                            /label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W19887;
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               R72068
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60 yaqkfqgrltitadeststaymelsslrsedtavyyca-gans-cnrsyyy--ymdvrgq 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EVQLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVPGAPGGGIEWMGGSISFFGTSN 60
                                                                                                                         This projected sequence comprises the heavy chain variable region (VH), HBAll, obtained by mutagenesis of the VH CDR3 of human carcinoembryonic antigen (hEA)-specific antibody 'CEA' (see THIOR) and specific binding member (A) comprises an hEA specific antibody antigen binding domain that has a dissociation constant for hEBA of less than 1 x 10 -8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 extracellular domain of hEBA and/or to cell-associated hEBA over hCEA over soluble hCEA. Preferred (A) include pairings of VH and VL sequences from (FAI)-7 (see W1986-95) or their CDR sequences, as well as CEAG VH ushutgenesis or chain shuffling. (A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 14; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                             iagnosing cancer, e.g. adenorarcinoma of the colon, lung or breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Specific binding members for human carcinoembryonic antiqen - bind to the A3-B3 extracellular domain of hCFA and are substantially non-cross-reactive with human liver cells; used for diagnosing
                                 Specific binding members for human carcinoembryonic antigen - bind
                                                     to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 593; DB 23; Length 123; Pred. No. 8.68e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-DEC-1997 (first entry)
CEA-specific antibody CEA6 VH sequence.
Carcinoembryonic antigen: CEA; human; antibody: scFv;
tumour marker; lung cancer; breast cancer; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note- "complementarity determining region 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note- "complementarity determining region 2"
Region
Osbourn JK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OSPOUTE JK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CAMR-) CAMBRIDGE ANTIRODY TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18
                                                                                                             Claim 4; Fig 2; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 64.8%;
Best Local Similarity 71.1%;
Matches 91; Conservative
McCafferty JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adenocarcinoma; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Allen DJ, McCafferty 10.
WPI: 97-319779/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-0CT-1995; GB-021295.
07-DEC-1995; GB-025004.
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Allen DJ, McCaffe.
WPI; 97-319779/29.
                                                                                                                                                                                                                                                                                                                                                                                            123 AA;
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12-JUN-1997.
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                                                                                             cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVQLLEQSGAEVKKPGSSVKVSGKASGGTFSGHVISWVFQAPGG I FWMGGSISFFGTSN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 gyglv-gsgaevkkpgssvkvsckasggtfsnspinwlrgapggglewmgslipsfgtan 59
                                                                                                                                                              A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 - 8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 extracellular domain of hCEA and/or to reall-associated hCEA over hCEA and/or to reall-associated burse of hUEA over soluble hCEA. Preferred (A) include pairings of VH and VL. WH and VL variants, including combinations of CEAB VH with VL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This polypeptide sequence comprises the heavy chain variable region (VH), HBB6, obtained by mutagenesis of the VH CDR3 of human carcinoembryonic antigen (hCBA)-specific antibody CBA6 (see
                                                                                                                                                                                                                                                                                                                                                                                                                         regions from CEA6, Togod, Togos, Tokol2, Tokor, Tok
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Specific binding members for human carcingembryonic antiquent bind to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing
Claim 4; Fig la; 128pp; English.
This polypeptide sequence comprises the heavy chain variable region (VH) of human carcinoembryonic antique (hCEA)-specific antibody CEA6. WH 772125-52) and VL (T72138-55) gene sequences were obtained for anti-hCEA antibodies CEA1-CEA7 (see W19876-85).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carcincembryonic antigen; CEA; human; antibedy; scFv;
tumour marker; lung cancer; breast cancer; colon cuncer;
adenocarcinoma; diagnosis.
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CEA-specific antibody CEA6 VH mutant HBB6 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 592; DB 23;
Pred No 1 06e-39;
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Region 50..66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Osbourn JK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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W19889 standard; Frotein; 123 AA.
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123 AA;
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71.18;
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Les 91; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31,.35
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                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLIEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVRQAPGQGLEWMGGSISFFGTSN 60
                                                                                                                                                                                                                                                                                                                           5; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Specific binding members for human carcinoembryonic antigen - bind to the A3-B3 extracellular domain of hCEA and are substantially
Specific antibody antigen binding member (A) comprises an hCFA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 - 8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 extracellular domain of hCEA and/or to cell-associated hCEA over Neba or soluble hCEA. Preferred (A) include pairings of VH and VL sequences from CEA-7 (see W19876-85), or their CPB sequences, as well as CEA6 VH and VL variants (see W19886-95) obtained by mutagenesis or chain shuffling. An example of a claimed pairing is HBB6 VH with CEA6 VL. (A) is used to detect cells expressing hCEA, in vivo or in viltro, especially tymour cells for disgnosting cancer, e-q. adenocarcinoma of the colon, lung or breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-cross-reactive with human liver cells; used for diagnosing
                                                                                                                                                                                                                                                                                   Secre 591, DR 23, Length 123,
Pred. No 1,286-30.
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Region
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Pegion
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                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 71.1%;
Matches 91; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-DEC-1995; GB-025004.
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11-OCT-1996; GB-0213
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                                                                                                                                                                                                                                             123 AA;
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                                                                                                                                                                                                                                               Sequence
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A human anti-Varicocalla coster virus monoclonal antibody was prepd.
using the trioma method of Ostberg et al. (1983) Hybridoma 2:351-357.
One resultant trioma neutralised VZV in the absence of complement.
This cell line, designated cell line 109.8849, produced an antibody genes cell line, designated 938A9 cDNA, for the light and heavy chain variable region heavy chain (gamma-1) and two light chain (kappa) specific clones sequence 147 AA.
                                                                                                                                                                                                                                                               1 EVELLEGSSTAEVKKPESSSVKVSEKASSSTFSGHVISWVPGAPGEST EWMGGSISFFGTSN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 qvqlv-qsgaevkkpqssvkvsckasgqtfsnfaiswvrqapggglewmgrimplfvtst 78
                                                                                                                                                                                                                              1 qvqlv-qsqaevkkpgssvkvsckasggtfsnspinwlrqapgqglewmgsilpsfgtan 59
                                                                                                                                                                                           J, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 18; Indels 6; Gaps
hoth over soluble hoth Preferred (A) include pairings of VH and VL sequences from CEA1-7 (see W19475-85) or their OFP sequences. as well as CEA6 VH and VL variants (see W19886-95) obtained by mutagenesis or chain shuffling. Examples of claimed pairings are lifely VH with locklic or CEA5 VL. (A) is used to detect ceils expressing hoth in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g adenorarinoma of the colon, lung or breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Varicella zuster virus, VZW; anti-VZW monoclonal antibody, 93KA9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93KA9 anti-Varicella zoster virus antibody heavy chain variable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human monoclonal antibodies specific for the glyco:protein II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sub.unit of varicella moster virus . used in a therapy and prophylaxis of infection
                                                                                                                                                        Score 588; DB 23; Length 123;
Pred No 2 31e-39;
16, Mismatches 16; Indels 1
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75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         r 10
R65019 standard; Protein; 147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glycoprotein II subunit; vaccine
                                                                                                                                                        Match 64.3%;
Local Similarity 71.1%;
les 91, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-OCT-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 70.2%;
nes 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SANO ) SANDOZ PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JUL-1994, U08241.
28-JUL-1993; US-098479.
24-MAP-1994; US-217918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ostberg L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lake P, Ostberg L;
WPI; 95-090612/12.
                                                                                                                         123 AA;
                                                                                                                                                                                                                                                                                                                                                                      116 gtmvtvss 123
                                                                                                                                                                                                                                                                                                                                                                                                       121 GTLVTVSS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; 082750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= CDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                           Sequence
                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                               Matches
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same type as the patient's tumour; (c) removing extraneous antibodies by absorption against normal human cells; (d) cloning the phage selected in step (b) and (c); (e) assaying the specificity of the cioned phage by incubating the phage with at least two types of cultured normal cells; and (f) further testing the specificity of cloned phage that do not bind to either cell line of cultured normal cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to cultured tumour cells derived from more than one other tumour that is not the patient's tumour. The present sequence represents a human heavy chain antibody, from a VH antibody fusion phage library, produced by a method as described above. The antibodies produced can be used for diagnostic and therapeutic applications and for isolating tumour antigens for studying tumourigenesis or for use as anti-cancer vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 19; Page 75-76; 82pp; English.

A process for isolating and synthesising human monoclonal anti-tumour antibodies has been produced. The process involves: (a) constructing at least one fusion phage library from the peripheral blood lymphocytes (PBLs) of a cancer patient; (b) screening for anti-tumour antibodies in the phage library in a binding assay with cultured tumour cells of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The human antibodies have low immunogenicity in humans compared to murine monoclonal antibodies (MAbs). Since the antibodies are isolated from fusion phage libraries, their affinity and specificity for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 rvtitadkststaymelsslrsedtavyyca····r·ygyr·ydaf·diwyggtlvtvs 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 RVSITADESASTAYMELSSLRSEDTAIYYCAKDPPRFCSGGNCYPGFFQQGGILVTVS 127
                                                                      79 yaqkfqgrvtisadaststaymelsslrsddtamyycardita--pgaaptplnfygmdv 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 gglevkkpgssvkvsckasggtfssyaiswvrqapggglewmggiipifgtanyaqkfgg 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 SGAEVKKPGSSVKVSCKASGGTFSGHVISWVRQAPGQGLEWMGGSISFFGTSNSAQKFQG 67
1 EVQLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVRQAFGQGLEWMGGSISFFGTSN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 8; Gaps
                                                                                                                                                                                                                                                                                                                                     28-OCT-1997 (first entry)
Anti-melanoma antibody 2-71 from VH antibody fusion phage library.
Human; monoclonal antitumour antibody; peripheral blood lymphocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prodn. of human monoclonal anti-tumour antibodies - by screening
fusion phage library produced using peripheral blood lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 584; DB 23; Length 119;
Pred. No. 5.06e-39;
11; Mismatches 9; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour cell line can be improved by genetic manipulations.
                                                                                                                                                                                                                                                                                                                                                                                                         cancer; tumourigenesis; anticancer vaccine.
                                                                                                                                                                                                                                                                   T 11
W13536 standard; protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R54795 standard, peptide, 120 AA. R54795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 63.8%;
Best Local Similarity 76.9%;
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JAN-1997.
28-JUN-1996; IB1032.
30-JUN-1995; US-497647.
(UYYA.) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from a cancer patient
                                                                                                                                               137 wgggttvtvss 147
                                                                                                                                                                                               118 WGQGTLVTVSS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 97-109061/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Garen A;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 s 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 S 128
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                                                                                                                                                                                                                                                                                                                W13536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
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60 aqifqqavtittdeststaymevsslrsedtalyycareqrrm-ai-n--p--fdywqqq 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stimulating produ. of variable region wene family restricted antibodies - through B-cell super-antigen vaccination bischosure; Page 77: 130pp; English.
A B-cell superantigen (sAg) is a fragment of SpA D domain that specifically binds the Fab portion of Variable region restricted antibodies. The sAg is used to enhance production of WH, especially VH3, restricted Abs. During attempts to identify sAgs, as sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l vglv-gsgaevkkpgssvkvtckasgdtfsssaiswvrgapgeglewmggiipifgtpny 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VQLLEQSGAEVKKPGSSVKVSCPASCGTPSCHVISWVPQAPGGGTEWMGGSISPFGTSNS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Gaps
                                                                                                                                                                                                                                                                                                                                              (R54784-801) of H chains from Ig reactive with mod-SgA, and aa and DNA sequences (R54802-15, 064842-56) of VH regions of SpA binders obtained from combinatorial libraries were determined. IgM protein BOR is derived from the germline configuration of a VH gene
              SpA-reactive lgM heavy chain clone BOR.
SpA domain D: 19 binding region: 19M: B-cell superantiquen; SAQ:
superantigen; heavy chain variable region; VH3 restricted antibody:
VH; protein-A: BOR: B-lymphocyte; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Graves' optibal mopathy-associated monorlonal antibody - produced by molecular cloning of immunoglobulin genes by PCK bisclosure: Page 69, 94pp: English.
L- and H-chain DNA was amplified by PCP from Graves' orbital tissue and clones encoding autoimmune-associated immunoglobulin fragments were obtained 12.15 clones of H chain (1961) genes showed homology to the closest germline genes, IPPI (2004-27) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HV1263 VH region.
Graves cphthalmopathy associated immunoglobulin protein;
orbital antigen; monoclonal antibody, heavy chain; H chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9; Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 578; DB 9; 1
Pred. No. 1.64e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NICH-) NICHOLS INST DIAGNOSTICS.
Mclachlan SM, Rapoport B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R72069 standard; Protein; 98 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       variable region; autoimmunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-SEP-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.48;
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 72.4%;
Matches 92; Conservative
                                                                                                                                                         30-0CT-1992; US-969936.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-124469.
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                                                                                                                                            29-OCT-1993; U10555
                                                                                                                                                                                                                                                                                                                                                                                                                                            120 AA;
                                                                                                                                                                                                             WFI, 94-167127/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; Q89328
                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                Silverman GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 - SEF - 1993;
                                                                                                                         11-MAY-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9508336-A.
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 18-0CT-1994
                                                                                                        W09409818-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               sedment.
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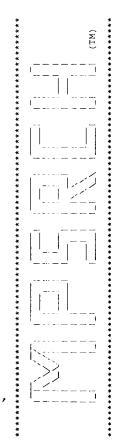
(GENP-) GENPHARM INT INC.

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1 gvqlv-gsgaevkkpgssvkvsckasgqtfssyaiswvrqapgqqlewmgriipilgian 59
                                                                                                                                                                                                                1 EVÜLLEĞSĞAEVKKPĞSSVKVSCKASGCIFSGHVISWVRQAPGÇGLEWMGGSISFFGISN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 gvglv-gsgaevkkpgssvkvsckasggtfssyaiswvrqapggglewmgriipilgian 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVOLLEQSGAEVKKPGSSVKVSCKASGGTFSGHVISWVRQAPGQGLEWMGGSISFFGTSN 60
                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PDSB: 022419.
Immunoglobulin trans:genes - for prodn. of heterologous firmunoglobulin trans:genes - for prodn. of heterologous non-rearranged and/or rearranged ig chains
Example 14: Page 87: 172pp: English.
The human placental genomic DNA library cloned into the phage vector lambda FIX II was screened with the human VHI family specific oligonucleotide (see 022418). Phage clone lambda 49.8 was isolated and a 6.1 kb xbai fragment contg. the variable segment VH49.8 subcloned into pNN03 to generate plasmid pVH49.8.
An 800 bp region of this insert was sequenced. VH49.8 was found to have an open reading frame which encoded the sequence shown.
(R72070) sequences of the VH region of a representative clone, OF7H1.2, are provided.
                                                                                                                                                                                                                                                                                                                                                                                        17-AUG-1992 (first entry)
Protein encoded by the human heavy chain V region gene VH49.8.
Heavy chain; variable region; VH1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 560; DB 4; Length 117;
Pred. No. 5.55e-37;
11; Mismatches 7; Indels
                                                                                                                  Length 98;
                                                                                                               Score 500; DB 12, Length 98, Pred. No. 5.55e-37; 11; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 yaqkfqgrvtitadkststaymelsslrsedtavyycar 117
                                                                                                                                                                                                                                                       60 yaqkfqgrvtitadkststaymelsslrsedtavyyrar 98
                                                                                                                                                                                                                                                                           61 SAQKFQGRVSITADESASTAYMELSSLRSEDTALYYGAK 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SAQKFQGRVSITADESASTAYMELSSLRSEDTAIYYCAK 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-NOV-1993 (first entry)
Human heavy chain V region VH49.8.
Immunoglobulin; 1gG; heavy chain; n
isotype switching; H chain variable
                                                                                                                                                                                                                                                                                                                                                            R22358 standard; Frotein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R38523 standard; Protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.8%;
Matches 80; Conservative
                                                                                                                 / Match
Local Similarity 80.8%;
Les 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENP-) GENPHARM INT INC.
Lonberg N, Kay R;
WPI; 92-113962/14.
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US-853408.
US-904068.
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29-AUG-1990; US-574748
31-AUG-1990; US-575962.
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                              ivī263 (089328).
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WO9203918-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
W09312227-A.
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                                                                                                                      Query Match
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                                                                                                                                    Best
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20 gygly-gsgaevkkpgssykysckasggtfssyaiswyrgapggglowmgriipilgian 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                      Example 12; Page 96; 196pp; English.
A human placental genomic DNA library cloned into the phage vector lambda FIX II was screened with mean VHI family specific ollygonuclectide Q44184. Phage clone lambda 49.8 was isolated and a
                                                                                                                                                                                                                                                                    6.1kb Xbal fragment containing the variable segment VH49.8 was subcloned into pNNO3 to generate plasmid pVH49.8. An 800bp region of this insert was sequenced (Q44185) and VH49.8 found to have an open reading frame and intact splicing and recombination signals, indicating that the gene is functional. Amino acid sequence Q44185 was deduced from the coding sequence; the last 3
                                                                                             chain
                                                                                                                                                                                                                                                                                                                                                                                                                             codons before the termination codon have not been translated. Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Owery Match 61.2%; Score 560, DB 7; Length 117, Best Local Similarity 80.8%; Pred. No. 5.55e-37; Matches 80; Conservative 11; Mismatches 7; Indels
                                                                                           Transgenic non-human animals contg. immunoglobulin heavy o
trans gene - used to produce useful antibodies by isotype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SAÇKFÇGEVSITADESASTAYMELSSLESEDTALYYCAK 99
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Job time : 37 secs.
                     Lonberg N;
                                          i; 93-214169/ž6.
                                                                     N-PSDB; Q44185.
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                     Kay RM,
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Release 2 10 John F Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U K Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tup Pah 24 07-04-15 100A; MasPar time 5 78 Seconds 465.989 Million cell updates/sec Tabular cutput not generated. Pun on.

(1-127) from US08844215 pep 931 >US-08-844-215-2 Description: Perfect Score:

1 EVQLIJEQSGAEVKKPGSSVK.

....HIMGYYFDYWGQGTLVTVSS 127

PAM 150 Gap 11 Scoring table: Sequence.

59021 seqs, 21210388 residues Searched:

Listing first 45 summaries Minimum Match 08 Post-processing:

swiss-prot34 Database:

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11

Mean 42 278; Variance 75.769; scale 0.558 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	21 22 28 33 25 24 4 4 4 4 5 1 2 2 3 2 2 1 4 5 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	
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ALIGNMENTS

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DISULFIDE BOND.
MEDLINE: 71064027.
GALL. W.E., EDELMAN G.M.;
BITCHEMISTRY 9-31386(1970).
--- THE SEQUENCE OF THE GAMMA-1 C PEGION OF THIS MYELOWA PROTEIN HAS ALSO REEN DETERMINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
                                                                                                             21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (PEL. 01, LAST SECTENCE UPDATE)
21-JUL-1986 (PEL. 01, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-I REGION (EU).
HOWO SAPIENS (HUMAN).
EUKARYOTA: METAZOR: CHOPPATA; VEPTEBRAIA: TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 58.3%; Score 543; DB 5; Length 117; Best Local Similarity 76.5%; Pred, No. 2.65e-93; Matches 75; Conservative 11; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE.
MEDLINE: 71064024.
MEDLINE: 71064024.
CUNNINGHAM R.A., BUTTSHAUSER H., GALL W.E., GOTTLIER P.D.
WAXDAL M.J., EDELMAN G.M.;
PIOCHEMISTRY 9:3161-3170(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYPPOLITIONE CAPPOXYLIC ACID

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        SEQUENCE
        137 Aa, 12472 MW; FCF9E17D CPC32;
        129032;

                                    117 AA
                                    PRT;
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HSSP; P01810; 1FVB.
IMMUNOGLOBULIN V REGION.
                                    STANDARD;
                               HV1A_HUMAN
P01742;
RESULT
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        11-JUL-1996 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-GT-1996 (REL. 44, LAST ANNOTATION UPDATE)
HOROGOVER CHAIN PRECIRSOR V-I PEGION (HG3)
HOROGOVER (HIMAN)
EUKRAYOTA: METAZOA; CHOPCAIA; VEFTERRATA; TETRAPUCA: MAMMALIA;
                                                                                                                                                                                                                                                                                                                                Score 491; DB 5; Length 117;
Pred. No. 1.10e-81;
13; Mismatches 16; Indels 1;
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MEDLINE: 88296408.
MATSUDA F., LEE K.H., NAKAI S., SATO T., KODAIRA M., ZONG S.Q., ONNO H. PUKUTARA S., HONJO T.;
EMBO J. 7:1047-1051(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA: CHOPDATA: VEPTERPATA; TETPAPODA; MAMMALIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 51.3%, Score 478; DB 5; Length 117; Best Local Similarity 67.7%; Pred No. 8 500-79; Matches 67: Conservative 11 Mismatches 20, Index)s
                                                                                                                              SEQUENCE FROM N A MEDIINE, 81144028.
MEDIINE, 8144028.
FECHAVI G., PAM D., GLAZER L., ZAKUT R., GIVOL D.; PROC. NATL. ACAD. SCI. U. S. A. 80.855-R59(1983).
EMRL: JOO240; G553411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YAQKFQGRLSITADDSTSTAYMELSSLRSEDTAVYFCAR 99
                                                                                                                                                                                                                                                                                   117 117
117 AA; 12945 MW; ECCEBIDE CEC32;
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01-NOV-1991 (PEI. 20, LAST SEQUENCE UPDATE)
01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
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HOMO SAPIENS (HUMAN).
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PIR; S00476; HVHU35.
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HSSP: P01810; 1FVR
IMMUNGLORULIN V REGION; SIGNAL
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IMMUNOGLOBUTUN V PEGTON; SIGNAL.
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Best Local Similarity 59.7%;
Matches 69; Conservative
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Match 50.2%; Score 467; DB 5; Length 120; Local Similarity 56.3%; Pred. No. 2.33e-76; ms 71; Cusservative 20; Mismatches 29; Indels 6; Gaps
                                                                                                                                                                    SIEKEVITZ M., GEFTER M.L. PRODEUR P., KIBLET R.,
MARSHAK- ROTHSTEIN A.;
EGR. A. ZMUNDL. 12-1923-1923.
-!- FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERNITATED GENES
- THAT HYBRIDIZE TO THIS ONE. THE AUTHORS CONCLUDE THAT ALL OF
THESE V REGIONS HAVE PEARPANGED TO THE SAME J SEMENNI, 142.
                                                                                                                                                                                                                                                                                                                                                                                    2 VQLLEQSGAEVKKPGSSVKVSCQVFCDTESPYTGWI RQAPGGGEWGNTIPVYNTPNY 6.1
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                                    21-JUL-1996 (PEL, OI, CPFATED)
21-JUL-1996 (PEL, OI, LAST SPORPENTE UPDATE)
21-JUL-1996 (PEL, OI, LAST ANNOTATION IPPLATE)
1G HEAVY CHAIN V PESION (36-65).
MUS MUSCHUS (MOUSE).
MUSCHUS (MOUSE).
EUKAYÜTA: METAZÖA: CHUEMATA; VERTEBRATA: TETKAPODA: MAMMALIA: EUTHERIA: PODENTIA:
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EUKARYOTA: METAZOA: CHOKDAIA: VERTEBRATA; TETRAPODA; MAMMALIA;
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                                                                                                                                                                                                                                                                             IMMUNOGLOBULIN V REGION: ANTIARSONATE ANTIBODY; HYBRIDOMA
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125 125
125 AA; 13579 MW; 6745C023 CRC32;
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01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-I REGION (MOT).
            120 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KOJIMA M., KOIDE T., ODANI S., GNO T.;
MOL. IMMINOL. 23:169-174(1986).
PIR, A02025, HVHUMO.
HSSE, F01772, 8FAB.
IMMUNOGLOBULIN V REGION.
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96
125
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HSSP; P01789; 6FAB.
                                                                                                                                           SEQUENCE FROM N.A.
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MEDLINE: 86203277.
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MARSHAK - ROind.
The T. IMMINOL.
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HV1F_HUMAN
RESULT 4
ID HV03_MOUSE
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                   60 ygprsqarftvtrdsstttvymeltalisadtaiyycarga-hysdtddsgtslgpwggg 118
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1 EVOLLEOSGAEVKKPGSSVKVSCQVFGDTFSPTTIQWLFQAPGGGPFWMGNTIPVYNTPN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Gaps
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MEDLINE; 83065234.
MENTEN H , MOLGARD H.V , HOUGHTON M., DEPRYSHIPE P.B., VINEY J RELL L.O., GOULD H.J.;
PROC. NATL. ACAD. SCI. U.S.A. 79:6661-6665(1982).
                                                                                                                                                                                                                                                                                                                    RENNICH H.H., JOHANSSON S.G.O., VON RAHR-LINDSTEOM H.;
INI IMMEDIATE HYPERSENSITIVITY: MODERN CONCEPTS AND DEVELLOPMENTS,
RACH M.K., ED., PP.L.-4S, MARCEL DEKKER, NEW YORK, (1978).
--- THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
                                                                                                                                                                                                           SUKARYOTA: METAZOA; CHORDATA; VEPTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                    IG HEAVY CHAIN V REGION (ND).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 458; DR 5; Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 2.28e-74;
24; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                  21-JUL-1986 (PEL. 01, CPEATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
IG HEAVY (HAIN PRECIPSOR V-I PEGION (ND) (FPAGMENTS).
HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   T -> V (IN REF. 2).
IH -> HI (IN REF. 2).
VG -> GV (IN PEF 2).
MISSING (IN PEF. 2).
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P01741;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V REGION (ANTI-ARSONATE ANTIBODY).
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6D605E13 CRC32;
                                                                                                                                PPT;
                                                                                                                                                                                                                                                                                                                                                                                   IMMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 VG
121 MI
143
16051 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match
Local Similarity 53.8%;
les 70; Conservative
                                                                                                                                STANDARD:
                                                                                                                                                                                                                                                                                                                                                              PIR; A02026; ElHUND.
HSSP; P01607; 1FGV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
121
143
143 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 gggttvtvss 143
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                                                                                                                                                                                                                      EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                          SEQUENCE OF 16-142.
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                119 tllivss 125
                                                                                     121 TLVIVSS 127
                                                                                                                               HV1C_HUMAN
P01744;
                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
MOD_RES
DISULFID
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CONFLICT
NON_TER
SEQUENCE
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SIGNAL
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79 ynekfkgkttltvdkssstaymglrsltsedsavyfcar---sh-y-yggsydfdywggg 133
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SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 evgl-ggsgaelvkagssvkmsckatgytfssyclywvrgapggglcdlgyissssaypn 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 evgl-ggsgaelvragssvkmsckasgytftsgjinwvkgrpggglewigyinpgngyin 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMUNOGLOBULIN V REGION; ANTTARSONATE ANTIBODY; HYRFIDOMA; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUS MUSCULUS (MOUSE).
EUKARYOTA, METAZOA; CHORDATA; VEPTEBPATA; TETRAPODA; MAMMALIA;
EUKAPYOTA: METAZOA; CHOPDATA; VERTEBRATA; TETPAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDITHE: 82152818.
SIMS J., RABBITTS T.H., ESTESS P , SLAUGHTEP C., TUCKEP P.W
CAPRA J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG HEAVY CHAIN V PEGION (93G7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 48.1%; Score 448; DB 5; Length 140; Local Similarity 55.9%; Fred, No. 3.68e-72; es 71; Conservative 20; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 456; DB 5; Length 114;
Pred No 6.31e-74;
13; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 yaqkfqgrvtitadcstntaymelsslrsedtavyfcavrvi 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YAQKFQGRLSITADDSTSTAYMELSSLRSEDTAVYFCA-RVV 101
                                                                                                                                                                                                                                                                                                                               IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY
                                                                                                                                                                                                                                                                                                                                                          NON_TER 114 114
SEQUENCE 114 AA; 12555 MW; 1A027FID CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 AA; 15514 MW; 0700D5C8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
10-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PPECURSOP V PEGION (93G7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 AA.
                                                                                                   STPAIN=A/J;
MEDLINE; 79195438.
CAPRA J.D., NISONOFF A.;
J. IMMUNOL. 123:279-284(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 19.0%;
Local Similarity 69 6%;
les 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCIENCE 216:309-311(1982).
EMBL; J00493; G195007; -.
PIR; A02028; HVMSG7.
HSSP; P01789; 6FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                      SEQUENCE.
PIR, A02022; G1MSAA.
HSSP; P01772; 1FGV.
                        EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUTHERIA; RODENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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79 ynekfkskailtvdkpsstaymqissitsedsavyycar--y-d-y-ygssy-fdywggg 132
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                                                                                                                                                                     RATEWSKY K.,
                                                                                                                                                                                                                                                                                                            IG HEAVY CHAIN V REGION (B1-8 / 186-2).
                                                                                                                                                                                        CELL 24:655-637(1991).
-!- THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYRPIDOMA MAKING
-!- THE B1-8 TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB
ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB
PRI; 139 AA.
P01751; P01752;
21-J01-1986 (REL. 01, CREATED)
21-J01-1986 (REL. 01, LAST SEQUENCE UPDATE)
C1-UT1-1996 (REL. 34, LAST ANN-TAITUN UPEALE)
IGHEAVY CHAIN PRECUPSOR V PEGTON (R1-8 / 186-2)
BUS NUSCUUS (MOUSE).
EUKARYOTA: METAZOA: CHORDATA: VERTERRATA: TFTRARODA: MAMMALIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA; CHORDATA; VERTERRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                      FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                                           COMPLEMENTARITY-DETERMINING 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 4%; Shore 42%; DR 5; Length 139;
51 2%; Prod No 1 160-66;
aftive 27; Mismatches 28; Indels
                                                                                                                                                        MEDLINE; 81234548.
ROTHWELL A L.M , PASKIND M , RFTH M , IMANISHI-KAPI T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-JAN-1940 (REL. 16, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PRECURSOR V REGION (VHSS8 AL/A4).
                                                                                                                                                                                                                                                                                                                                                                                                                                     15419 MW: DEB2C7DA CPC32:
                                                                                                                                                                                                                                                                                                                                                                                                 SEGMENT.
                                                                                                                                                                                                                                                                                                                                                                         FRAMEWORK 3.
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SIGNAL 1 19 19
CHAIN 20 139
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CELL, 40.271-281 (1985).
EMBL; M13787; G466291; -..
PIR; A02029; HVMSA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 51 2%;
les 65; Conservative
                                                                                                                                                                                                                                              J00529; G195115; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                             EMBL; J00529; Ğ195115
PIR; A02034; MHMS18.
HSSP; P01810; JJHL.
                                                                                                                                                                                                                                                                                                                                                                                                             41
139
139 AA;
                                                                                                      EUTHERIA; RODENTIA.
                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                  ANTIBODIES).
                                                                                                                                                                                                                                                                                                                      20
55
55
69
86
118
                                                                                                                                             STRAIN-C57BL/6
                                                                                                                                                                                 BALTIMORE D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LT 10
HV52_MOUSE
P06327;
                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
SEQUENCE
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DISULFID
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Query Match 44.1%; Score 411; DB 5; Length 119; Sest Local Similarity 50.0%; Pred. No. 4.90e-64; Aatches 64, Conservative 31; Mismatches 23; Indels 10; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 gyglv-gsgggvygpgrslrlscaasgftfsrytihwvrgapgkglowva-vmsybybbk 58
                                                                                                                                                                                                                                                                                                                                                                                                                              20 gygl-ggsgpelvkpgalvkisckasgytftsydinwykgrpugglewidwiypeddst.k 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EVOLLEGSGAEVKKPGSSVKVSGQVFGFTFSFYTIGMLRGAPGGGFFWMGNIIPVYNIPN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVOLLEUSGAEVKKPGSSVKVSCOVFGIVTFSPYTTOWTPOAPGOGPEWMGNITPVY-NTP 59
                                                                                                                                                                                                                                                                                                                                                                           Saps
                              IS BEAVY CHAIN V REGION (VBSSR ALZA4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; METAZGA: CHORDATA; VEKTERRATA; TETRAPODA; MAMMALLA;
EUTHERTA; PRIMATES.
                                                      FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
                                                                                                                           COMFLEMENTARITY DETERMINING 2. PPAMEWORK 3.
                                                                                                                                                                                                                                                                                                               / Match 44.1%; Score 411: DB 5: Length 117: Local Similarity 56.6%; Pred. No. 4.90e-64; es 56, Conservative 20, Mismatches 22, Indels
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DPEKER L , SCHWART J, PRICHEL W , HILSCHMANN N.;
HOPPE-SEYLER'S Z, PHYSIOL CHEM 347:1515-1540(1976),
I-THIS CHAIN WAS ISOLATED FPOM AN 1GG1 MYELOMA PROTEIN,
PIR; A20053; GHUNI.
HSSP; POLGOT, LEGV.
IMMUNGIORULIN V PEGION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYRROLIDONE CARBOXYLIC ACID.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YAUKFUGKLSIIADDSISIAYMELSSLRSEDIAVYFTAR 99
                                                                                                                                                                                                                                                         12971 MW; A60F2B13 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 AA; 13242 MW; 5703CA8E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (PRI 01, IAST SEQUENCE UPDATE)
21-JUL-1986 (PEL 01 IAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 AA
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                                                                                                               FRAMEWORK 2.
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HOPPE-SEYLER'S 2 PHYSTOL CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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688
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1115
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P01770;
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ID HV1D_HUMAN
AC P01760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOD_RES
DISULFID
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SEQUENCE
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DISULFID
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SEQUENCE
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19 yeokfubailtudksstaymqlsslipeofauyyoar---sdgy-y--dw-fvywagg 131
                                                                                                                                                                                            61 YAQKEQGRLSITADDSTSTAYMELSSLPSEDTAVYFCAPVVIPNAIPHTMGYYFDYWGQG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STPAIN=CS7BL/6;
MEDLINE: 81234548.
ECTHWELL A L.M., PASKIND M., PETH M., IMANISHI-KAPI T , PAJEWSKY K ,
                                                     20 ergliggspolykpgasykisckasgytftdynmhwykgshgkslewigylyp-ynggt 77 (m. 1914) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVÖLLEDSSAEVKKPESSVKVSGGVPGFFFSPYTTGWLFGAPGGGPEWMGNIIPVYNT-P 59
                             20 gygl-gapgaelvkpgasyglsckasghtftnywihwvkgrpggglewigeinpndgrsn 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 408, DB 5; Length 117;
Fred No 2.22e-63,
21: Mismatches 20; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BALTIMORE D.:
CELL 24 (525-637 (1981).
-1- 141S GEMELINE GENE BELONGS TO A SET OF CLOSELY KELATED GENES
THAT COULD ENGOBE V FEGIONS OF NPR ANTIRODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUS MUSCULUS (MOUSE).
EUKAPYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUS MUSCULUS (MOUSE).
EUKREKOTA, MELAZOA, CHOFDATA, VEPIERRATA; TETRAPODA: MAMMALLA;
EUTHERIA: RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECURNCE FROM N A MEDIINE, 81245215.
SIVAL E., EARTH P., EFFRON K., PECHAVI G., FAM E., CCHEN T B. NATURE 292-426-430(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IG HEAVY CHAIN V REGION (10A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 gysgkfkskatltvånssstaymelssltsodsayyydar 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 NYAQKFQGRISITADDSTSTAYMELSSLPSEDTAVYFCAR 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 117
117 AA; 12972 MW; 941C002E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                  17 14
HV14_MMUSE STANDARD; PRT; 117 AA HV14_MMUSE
101758; 21-701.1986 (PEL. 01, CREATED)
21-701-1986 (REL. 01, LAST SEQUENCE UPDATE)
1-071-1996 (PEL. 34, LAST ANNOTATION SEDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
11-NOV-1990 (PEL. 16, LAST ANNOTATION UPDATE)
1G HEAVY CHAIN PRECUESOR V REGION (102).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG HEAVY CHAIN PRECUESOR V REGION (108A).
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMUNOGLOBULIN V REGION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 43.8%; Local Similarity 56.0%; es 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HVO6_MOUSE STANDARD;
P01750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J00488; G554028; -.
PIR; A02041; HVMS8A.
HSSP; P01789; 11GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIP; ACECAE; HVMSC;
HSSP; PO1810; LUHL
                                                                                                                                                                                                                                                           132 tlvtfsa 138
                                                                                                                                                                                                                                                                                                                 121 TLVTVSS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Mismatches 18; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLLEQSGAEVKKPGSSVKVSCQVPGUTPSPYTI_WLPLAPS_GPEWM3N1[PVYNTPN 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDILINE: 84248078.
GILLIAN A.C., SHEN A.C. PICHAPDS J.E., BLATTNEP F.P., MISHINSKI J.F.,
TUCKEP P.W.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 gvglm-gsgaevkkpgssvrvscktsggtfvdykglwvrgapgkglewvggiplrfngev 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG HEAVY CHAIN V REGION (TEPC 1017).
                                                                                                                                                                                                                                                                                                                                         -!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-0CT-1986 (REL. 02, CREATED)
23-0CT-1986 (REL. 02, LAST SEQUENCE UFDATE)
01-AUS-1992 (FEL. 23, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PPECTIES/PV PEXION (TEP? 1017).
MUS MUSCUUS (MOURE).
EUKARYCTA: METACOA; CHOPDATA; VEPTERBATA, TETPAPOGA, MAXMALIA.
                                                                                                                                            CHORDATA, VERTEBRATA, TETRAPODA, MAMMALTA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEMENTARITY-DETERMINING 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPLEMENTARITY - DETERMINING 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPLEMENTARITY - DETERMINING 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serro 409; DR 5; Longth 138;
Pred No. 1 34e-63;
26; Mismatches 99; radate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 411; DB 5; Length 124;
Pred. No. 4.90e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYFREGIFIENE CAPROXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROC NATL ACAD. SCI. U.S.A. 81-4164-4168(1984)
PR. ACADAS: HVMST7
HSSP. POL810: 1JHL.
IMMUNGLOBULIN V PECION; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES 1 1 PYFH-GIFF-NE CARRON NON_IER 124 124 SEQUENCE 124 AA: 13694 MW: 479BP2BE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 FPAMEWORK 4
115 RY SIMILABITY
138
15576 MW: BEF6247E CPC32:
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
13-JUL-1986 (PEL. 01, LAST SEQUENCE UPDATE)
15 HEAVY CHAIN V-1 REGION (WCL).
HOMO SAPIENS (HUMAN).
EUTHERIA: METALOA. CHOEDATA, VESTEBRATA. TETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAMEWORK 1
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                                                                                                                                                                                                                                               MEDIJNE; 82046599.
ANDREWS D W , CAPRA J D ;
BIOCHEMISTRY 20:5822-5930(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 98;
ilarity 50 48;
Conservative
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Best Local Similarity 55 1%;
Matches 70; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A02043; MIHUWL.
HSSP; P01607; 1FGV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUTHERIA: RODENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 tlvtvss 122
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NON_TER
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Best Local S
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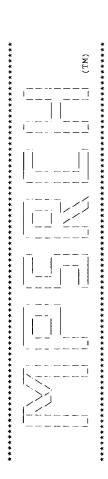
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Ouery Match
43.8%; Score 408; DB 5; Length 117;
Best Local Similarity 58.8%; Pred. No. 2.22e-63;
Matches 57; Conservative 18; Mismatches 21; Indels 1; Gaps
                                                                                                                                                                                                         IG HEAVY CHAIN V REGION (102). PRAMEWORK 1. COMPLEMENTATIY-DETERMINING 1. PRAMEWORK 2. COMPLEMENTARITY-DETERMINING 2. FRAMEWORK 3. BY SIMILARITY.
| 1 | 19 | 1G HEAVY CHAIN V REG | 20 | 117 | FERMEWORK 1. | 50 | 54 | COMPLEMENTARITY-DETE | 55 | 69 | 85 | COMPLEMENTARITY-DETE | 86 | 117 | FRAMEWORK 3. | 41 | 115 | 89 | SIMILARITY. | 117 | AA: | 12867 | MW: | 4BDD1982 CRC32;
  SIGNAL
CHAIN
DOMAIN
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Search completed. Tue Feb 24 07.04.30 1008 Job time: 24 secs.

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3



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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tie Feb 24 07-04:59 1998: MasPar time 8.21 Seconds 471.531 Million cell updates/sec Pun on:

Tabular output not generated.

>US-08-844-215-2 (1-127) from US08844215.pep 931 Description: Perfect Score:

1 EVÜLLEÇSGAEVKKPGSSVK Sednence:

. HIMGYYFDYWGQGTLVTVSS 127

PAM 150 Gap 11 Scoring table:

95051 seqs, 30469580 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:annl 2:ann2 3:ann3 4:ann4 5:unann1 6::nann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unann11 16:unann12 17:unenc 18:unrev pir53

Mean 41.781; Variance 118.597; scale 0.352 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred No.	46e-74 45e-74 11e-70	.08e-7 .12e-6 .18e-6	1.25e-68 5.95e-67 3.27e-67	.27e-6 .15e-6	15e-65 3.11e-64 1.31e-63 1.31e-63	10e-6 10e-6 10c-6
Description	Ig heavy chain V-1 r 1 Ig heavy chain V reg 1 Ig heavy chain V-1 r 1	g heavy chain V reg g heavy chain V reg g heavy chain V reg	g heavy chain V reg g heavy chain V reg g heavy chain V-1 r	g mu chain precu g heavy chain V- g heavy chain V	Ig heavy chain V reg 1 Ig heavy chain V-D-J 3 Ig heavy chain V reg 4 Ig heavy chain V reg 4	chain V
CI.	** 10 -*	10 10 10	PH0952 S46394 C33548	1468 4410 H095	50 C C	C. CLICLO
Length DB	227	C1 C1 C1	C1 CC CC	527 7 123 7 132 7	3112	8 9 9 9
Query				54.9 64.8 64.3	64.0 62.0 1.19.0	
Score	658 658 631	622 624 624	613 605 604	504 599	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	572 572 572 572
Result No.	404	4100	V 8 9	122	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	17 18 19 20

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120 ttvtrss 126 | | | | | | | | 121 TLVTVSS 127

17 55.5 160 7 F10105 anti-PR2 erythrocyté 2.030-5	17	
17 55.5 148 7 S29257 Ig heavy chain V reg 2.03e-5	17	
17 55.5 114 7 PH1667 Ig heavy chain V reg 2.03e-5	17	
18 55.6 108 7 PH1664 Ig heavy chain V reg 1.46e-5	18	
9 55.7 109 7 PH1671 Ig heavy chain	19	41
25 56.4 118 7 S35265 Ig heavy chain V reg 1.49e-5	C.I	
26 56.5 129 7 S36260 Ig heavy chain V reg 1.08e-5	26	
27 56.6 98 7 A30523 Ig heavy chain V-I r 7.77e-5	27	
29 56.8 118 7 PH1666 Ig heavy chain V reg 4.04e-5	29	
34 57 4 116 7 S31667 Ig heavy chain V reg 7 90e-5	34	
36 57.6 136 7 PN0536 IqG heavy chain V re 4.11e-5	36	
39 57.9 135 7 B32274 Ig heary chain precu 1.54e-5	39	
39 57.9 127 7 S34014 Ig heavy chain V reg 1.54e-5	39	
42 58.2 97 7 PHO870 Ig heavy chain V reg 5.78e-5	42	
43 58.3 117 2 GlHUEU IG heavy chain V-I r 4.16e-5	43	
45 58.5 123 7 D33548 Ig heavy chain V-1 r 2.16e-5	45	
49 59.0 122 7 S36271 Iq heavy chain V req 5.84e-5	4.9	
53 59.4 98 7 S46463 Ig heavy chain VI re 1.58e-5	53	
57 59.8 113 7 PH1663 Iq heavy chain V req 4.25e-6	57	
63 60.5 122 7 040590 Iq heavy chain V req 5 946-6	6.5	
65 60.7 124 7 S19665 Ig heavy chain V reg 3.08e-6	65	
70 61 2 121 7 A49590 Iq hoavy chain V roq 5 976-6	7.0	
70 51.2 98 7 S24680 Iq heavy chain VI re 5.97e-6	70	
72 61.4 142 7 A32483 Ig heavy chain V reg 3.10e-6	72	
72 61.4 135 7 PH0953 Ig heavy chain V reg 3.10e-6	C)	

B33548 #type complete Ig heavy chain V-1 region (AND) - human #formal_name Homo sapiens #common_name man 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change		#journal Proc. Natl. Acad. Sci 17 S.A (1989) 84.5913-5917 #title Developmentally restricted immunoglobulin heavy chain variable region gene expressed at high frequency in chronic lymphocytic leukemia.	cession B3348 #*status preliminary; nucleic acid sequence not shown; not compared with conceptual translation ##molecule_type DNA ##residues 1-126 ##label KIP ##experimental_source the sequence was determined from the	differentiated gene TON *superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; immunoglobulin #domain immunoglobulin homology #label IMM #length 126 *molecular-weight 13710 *checksum 4068	Query Match Best Local Similarity 73.2%; Fred. No. 1.46e-74; Matches 93; Conservative 13; Mismatches 20; Indels 1; Gaps 1;	<pre>qvqlv-qsgaevkkpgssvkvsckasggtfssyaiswvrqapggqlewmgglipifgtan 59 : : </pre>
RESULT 1 ENTRY TITLE ORGANISM DATE	ACCESSIONS REFERENCE #anthors	#journal #title #cross-red	#accession #astatus ##status ##molecule ##experime	CLASSIFICATION KEYWORDS FEATURE 15-98 SUMMARY	Query Match Best Local Matches	Db 1 qvq : Qy 1 EVQ

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Developmentally restricted immunoglobulin heavy chain variable region gene expressed at high frequency in chronic lymphocytic leukemia.
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                                                                                                                                                                   #authors Martin, T.: Duffy, S.F. Carson, D.A.: Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies
#cross-references MUID:92202880
                                       Ig heavy chain V region (G6+ CLL-AND) - human (fragment)
#formal_name Homo sapiens #common_name man
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#journal J. Exp. Med. (1992) 175:983-991
#fitle Evidence for somatic selection of natural authoriticalises.
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1-129 ##label MAR
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heterotetramer; immunoglobulin
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#superfamily immunoglobulin V region; immunoglobulin homolody
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#formal_name Homo sapiens #common_name man
17.Apr.1993 #sequence_revision 17.Apr.1993 #foxt_change
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#journal J. Exp. Med. (1992) 175:983-991
#tille Evidence for somatic selection of natural antoantibodies.
#rrcs.references MUID-92202880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Martin, T.: Duffy, S.F.: Carson, D.A.: Kipps, T.J.
#journal J. Exp. Mcd. (1992) 175-383-991
Evidence for somatic selection of natural autoantibodies #cross-references MUID:92202880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 gvglv-gsgaevkkpdssvkvsckasgetfssyaiswvrgapgglewmggiipifgtan 59
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J. Exp. Med. (1992) 175:983-991
Evidence for somatic selection of natural autoantibadies
                                PHGGE2 **Type fragment

Ig heavy chain V region (G6+ T-L42) - human (fragment)

*formal name Home sapiens #common_name man

17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change

16-Aug-1996
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#domain immunoglobulin homology #label IMM\
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#length 120 #checksum 5559
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1-128 **label MAR *superfamily immunoglobulin homology *superfamily immunoglobulin V region: immunoglobulin homology
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#journal J. Exp. Mrd. (1942) 175-983-991
#title Evidence for somatic selection of natural autoantibodies.
                                                                                                                          1 quqlv-qsgaevkkpgssvkvsckasggtfssyalswvrqapggglewmgglipifgtan 59
                                                                                                                                                    PH0952 #type fragment Ig heavy chain V region (66+ CLL-SMI) - human (fragment) #formal_name Howe sapiens #common_name man 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
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Pred No 4.25e-68;
15; Mismatches 20; Indels 3; Gaps
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1g heavy chain V region - human
#formal_name Homo sapiens #common_name man
27.Jan-1995_#sequencc_revision 27-Jan-1995 *text_change
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Query Match 66.8%; Score 522; DB 7; Length 122;
Pest Lonal Similarity 73.2%; Prod No. 2.186 Fo;
Matches 93; Conservative 15; Mismatches 14; Indels
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#length 128 #checksum 3537
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115 -DYWGQGTLVTVSS 127

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Proc. Natl Acad Sci U S A. (1989) 86:5913-5917
Developmentally restricted immunoglobulin heavy chain
variable region gene expressed at high frequency in chronic
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FICATION #superfamily immunoglobulin V region, immunoglobulin homology
DS heterotetramer; immunoglobulin
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J. Mol. Biol. (1994) 239:68-78
In vitro assembly of repertoires of antibody chains on the
surface of phage by renaturation.
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#formal_name Homo sapiens #common_name man
17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
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#length 133 #molecular-weight 14320 #checksum 1289
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#length 132 #molecular-weight 14293 #checksum 7515
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Pred. No. 5.95e-67;
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#accession C33548
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Local Similarity 67.9%;
les 91; Conservative
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Local Similarity 68.4%;
les 91; Conservative
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Proc. Natl Ac
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##cross-references EMBL:X17115
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
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FICATION #superfamily immunoglobulin V region; immunoglobulin homolody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                816
                                    Ig mu chain precursor, membrane-bound (clone 201) - human
formal_name Homo sapiens #common_name man
31-bec-1991 #sequence_revision 31-bec-1991 #text_change
16-Aug-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 yaqkfqgrvtitadeststaymelsslrsedtavyycaktqilqpyssqwypnsdyyyyq 138
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                                                                                                                                                                              Friedlander, R.M.; Nussenzweig, M.C.; Ledor, P. Nucleic Acids Pes. (1990) 18:4278 Complete nucleotide sequence of the membrane form of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 qvqlv-qsgaevkkpgssvkvsckasggtfssyaiswvrqapqqqlewmqqilplfqtan 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Gaps
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#formal_name Homo sapiens #common_name man
13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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Pred. No. 8.27e-67;
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                   #type complete
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#cross-references MUID:90332450
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Best Local Similarity 67.9%;
Matches 91; Conservative
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1-132 ##label MAR #superfamily immunoglobulin homology
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Ig heavy chain V region (ACHSVI, clone 18) - human (fragment)
Heformal_name Homo sapiens #common_name man
06-oct-1994 #sequence_revision 18-Nov-1994 #text_change
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J. Exp. Med (1992) 175-983-991
Evidence for somatic selection of natural autoantibodies.
                                                                                                                                                                                        PH0954 #type fragment

Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
#formal_name Homo sapiens #common_name man
17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
1 qvglv-qsqaevkkpgssvkvsckasggtfssyaiswvrqapgqglewmggiipifgtan 59
                                    1 EVQLLEQSGAEVKKPGSSVKVSCQVFGDTFSRYTIQWLRQAPGQGPEWMGNIIPVYNTPN 60
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Recombinant human Fab to qlycoproteden D neutralizes
infectivity and prevents cell-to-cell transmission
herpes simplex viruses 1 and 2 in vitro.
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Pred. No. 4.30e-66;
16; Mismatches 19.
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Local Similarity 68.4%;
nes 91; Conservative
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##residues 1-122 ##label BUR
##cross-references NCBIP:141851
##experimental_source hone marrow lymphocytes
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##note sequence extracted from NCBI backbone
##INOTE ##INOTE
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FICATION #superfamily immunoglobulin V region; immunoglobulin homology
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#formal_name Homo sapiens #common_name man 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 16-Aug-1996
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12, Mismatches 21, Indels
                                                                                                                                                                                                               Length 122
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17, Mismatches 18;
                                                                                                                                                                                                               64.0%; Score 596; DB 7;
                                                                                                         heterotetramer; immunoglobulin
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Best Local Similarity 70.9%;
Matches 83; Conservative
                                                                                                                                                                                                                                   Best Local Similarity 69.4%;
Matches 86; Conservative
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                                                                                      CLASSIFICATION
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S36256
Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.;
Embleton, M.J.; McCafferty, J.; Baier, M.; Holliger, K.P.;
Gorlck, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.R.; Winter,
                                                                                                                                                                                         3;
                                                                                       EMBO J. (1993) 12:725-734
Human anti-self antibodies with high specificity from phage
display libraries.
S36261
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                                                                                                                                                                                                                                                                                                                                      Query Match 62.1%; Score 578; DB 7; Length 116;
Best Local Similarity 69.5%; Pred. No. 4.31e-63;
Matches 82; Conservative 14; Mismatches 19; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##status preliminary; nucleic acid sequence not shown ###modecule_type mRNA
                                                                                                                                                                                                                                                                                    #domain immunoglobulin homology #label IMM #length 116 #checksum 7971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: Tue Feb 24 07:05:34 1998 Job time: 35 secs.
                                                                                                                                                #accession
                                                                                          #journal
#title
                      #authors
   REFERENCE
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FEATURE
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Release 2.1D John F. Gollins, Biocomputing Pescarch Unit Copyright (c) 1997, 1994, 1995, University of Edinburgh, U.K Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tup Feb 24 07 33.22 1998. MasPar time 3.39 Seconds 190.958 Million cell updates/sec From Other

Tabular output not generated.

>US-08-844-215-2 (1-127) from US08844215.pep 931

HIMGYYFDYWGQGTLVTVSS 127 1 EVQLLEQSGAEVKKPGSSVK Description: Perfect Score: sedneuce:

PAM 150 Gap 11 Scoring table:

56402 seqs, 5095871 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-issued 1.backi 2.51 3.52 4 53 5.54 6.55 7.56 8.PGT90 9.PGT91 10-PGT92 11-PGT93 12-PGT94 13-PGT95 14-PGT94

Mean 29 297; Variance 150,259; scale 0 189 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length	Ę.	II	Description	Pred. No.
	1	66.2		<u>رح</u> .	-212-80-51	Sequence 4, Application	65.454.8
CI	()	64.7	120	H	PCT-US93-1	12, Applica	ω. ω.
æ	583	62.6	129	23	-0895-	45, Applicat	
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11	4	œ.	140	11	PCT-US93-1	12,	1.19e - 33
15	7	မှ အ မာ	E C	7	US-08-264-	3,	1 710.23
13	4	σ.	121	<u></u>	PCT-US93-1	α,	7
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16	4	ربر (د)	r: 4	ټ.	183.10.31	•	Ç.
17	4	ω,	117	9	-08-4	15	
18	4	ω.	Н	9	-07-63	Н	
19	543	ω,	117	7	US-08-487-	15	
20	4	58.3	117	7		Sequence 104, Applicat	
21	4	œ.	117	7	US-08-487-		5.9
CI	ربا درا	(C)	[- 1 - 1	۲.	US-08-474		33

BUNGLIGES

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Sequence 72, Application Sequence 72, Application Sequence 72, Application Sequence 73, Application Sequence 13, Application Sequence 53, Application Sequence 53, Application Sequence 11, Application Sequence 11, Application Sequence 11, Application Sequence 12, Application Sequence 16, Application Sequence 11, Application Sequence 12, Application Sequence 13, Application Sequence 14, Application Sequence 15, Application Sequence 15, Application Sequence 16, Applicat	
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ALIGNMENTS

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COPPESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible UFBRAIN SYSTEM: PC-PUSZ/MS-DOS SOFTWARE PARGOITE PARGOSE #1.0. Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                         APPLICANT: LAKE, PHILIP
AFFLICANT CSTRENG, LARS
TITLE OF INVENTION: HUMAN ANTIRODIES AGAINST
TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS
NUMBER OF SEQUENCES: 4
        147 AA.
                                                                                                                                                                                                                                                                                                                 FILLNS DATE: 24-MAR-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
FRYE 147 AA, 17801 MW, 113306 CH;
          PRT;
                                                                                          Sequence 4, Application US/08217918
Patent No. 5506132
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Smith, Willaim M
REGISTRATION NUMBER: 30,223
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 226-2403
INFORMATION FOR SEQ. 10 NO. 4.
                                                                       Sequence 4, Application US/08217918.
                                                                                                                                                                                                   379 Lytton Avenue
                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 147 amino acids TYPE: amino acid
          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                     COMPUTER PEADABLE FORM-
MEDIUM TYPE. Floppy
                                                                                                                                                                                                              Palo Alto
: California
RY: US
                                                                                                                                                                                                                                 COUNTRY: US
  T 1
US-08-217-918-4
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                                                  01-JAN-1900
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RESULT
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VARIABLE PEGION GENE FAMILY PESTRICIED ANTIROPIES
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                           'n
                                                                                                      79 YAQKFQGRVTISADASTSTAYMELSSLPSDDTAMYYCARDITAPGAAPTPLNFYGMLVWG 138
                                                                                                                             61 YAQKEQGELSITADDSTSTAYMELSSLESEDTAVYFCAP-VVIPNAIPHTMGYY-FDYWG 118
                                                                  20 QVQLV-QSGAEVKKP3SSVKVSGKASGGTFSNPATSWVPQAPGGGLEWMGFIMPLFVTST 78
                            Gaps
Score 616, DB 6; Length 147,
Pred, No. 5.42e 39;
18; Mismatches 22; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                          METHOD FOR STIMULATING PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBRILE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TRM PC compatible
OPERATING SYSTEM: PC-POS/Ms-Dos
SOFTWARE: PatentIn Pelease #1 (), Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                   120 AA
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1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER. PCT/USG*/10555
29-00T-1993
                                                                                                                                                                                                                                   PPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Howells, Stacy L. REGISTRATION NUMBER: 34.842
REGISTRATION NUMBER: FD-2630
TELECOMMINICATION INFORMATION
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application PC/TUS9319555
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              Sequence 12, Application PC/TMS9310555
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LOCATION: 1 120
NOE 120 AA: 12044 MW: 80846 GN:
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                                                                                                                                                                                                                                   STANDARD
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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amino acid
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Query Match 65.2%;
Best Local Similarity 66.7%;
                           86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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CLASSIFICATION:
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MOLECULE TYPE:
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PCT-US93-10555-12
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60 AGKEGSPVIITTDESISTAYMEVSSI RSEDTAL/YYCAREGRRMAI-NP----FDYWGGGT 114
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                                                                                                                  1 Volv-gsgafvkkpgssvkvtgkasgdffssafswvpgapggglfwmgg1fplfgtpny 59
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bendig, Mary M.
APPLICANT: Leger, clivier J.
APPLICANT: Saldanha, Tose
APPLICANT: Jones S. Tarran
TITLE OF INVENTION: Homesized Antibudies Assined institute OF INVENTION: Adhesion Molecule VLA-4
tength 120;
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                                                          Indela
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 AA
                                                    14; Mismatches 16.
                                Pred. No. 6.85e-38;
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69.2%; Pred. No. 2.13e-36;
  PB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCHIMMES. CURRENT APPLICATION DATA:
APPLICATION NUMREP. PCT/HSGS/01219
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US UB/186,269
FILING DATE: 25-JAN-1994
ATTOPNEY/AGENI INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15270-14
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  Score 602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 45, Application PC/THS9501219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-FOS/MS-POS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
JENCE 129 AA; 13930 MW; 96169 CN;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ±0, 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
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Query Match
Best Local Similarity 72.28;
Matches 91; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER ÜF SEĞUENCES: 4
COPPESPONDENCE ADDPESS:
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California
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Bost Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                           122 LVTVSS 127
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1 VHLV-08GABVKKPGSSVKVSGKASGGIESSXAISWVFGAPGGGIEWMGGIIPIFGGANY 59
                                                            APPLICANT: THE SCRIPPS RESEARCH INSTITUTE INTLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HERPES TILLE OF INVENTION: SIMPLEX VIPUS AND METHODS THEREFOR NUMBER OF SEQUENCES: 25
85, Conservative 17, Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible oPPRATING SYSTEM: PC-FASA/WS-PAS SOFTWARP: Patentin Pelease #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/00067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2: Spensley Horn Jubas & Lubitz
1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                              F.F.3
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TELEPHONE: (619) 455-5100
TELEPAX: (619) 455-5110
INPORMATION FOR SEQ 1D NC: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., Lisa A.
PEGISTPATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                              STANDAPD;
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Rest Local Similarity 66-7%;
Matches 22, Consorvative
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California
RY: USA
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CLONE: FabhSV 8
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90067
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  Matches
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TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VAPIABLE PEGION GENE FAMILY PESTHICIED ANTIECDIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPEPANTIGEN AND CONTING
                                                                                                                                                60 NYAQKEQGPVTTTADTSTSTAYMBLSSLESBDFAVYYGAPAPGYGSGGGYERIKELVW 119
                                      1 QVQLV-QSGARVKKPGASVRVS-YRASAVTETSYAISWVBQAR-AGALEWMSWINPYSWRET 59 : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1] : [1
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  Matches 90; Conservative 11; Mismatches 25, Indels
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COMPUTER: IRM PC COMPATIBLE
OPERATING SYSTEM: PC-L05/MS-L05
SOFTWARE: Patentin Pelease #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              120 AA
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1880 Century Park East - Suite 500
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Pred. No. 4.40e-36;
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FILING DATE: 29-OCT-1993
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120 AA: 13008 MW; 78865 CN;
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NAME: Howells, Stacy L.
REGISTPATION NUMBER: 34,842
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Best Local Similarity 67.5%;
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MEDIUM TYPE: Floppy
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LOCATION: 1.120
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STATE: California
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                                                                                                                                                                                                       120 GOGTLVTVSS 129
                                                                                                                                                                                                                                              118 GOGTLVIVSS 127
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ID PCT-US92-10555-12
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Prod No 5 530-35;
14; Mismatches 26; Indels 1, Gaps
JMBER: PCT/US95/00067
04-JAN-1995
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SEQUENCE 122 AA: 12999 MW: 86643 CN;
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61 PODRIJITADVSTSTAYMOLSGLIYEDTAMYYCARVAYMLEPTVTAGG-LDVWGQGTTVT 119
                                     5 LEGSGAEVKKPGSSVKVSCOVFGOTFSPYILGWLRQAPGGGPEWMGNIIPVYNTPNYAGK 64
                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Recombinant Antibodies for Human Therapy NUMBER OF SEQUENCES: 114 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYSTEM: PC-DOS/MS-DOS
Patentin Release #1 0, Version #1 30
                                                                                                                                                                                                                                                                                                                                               ADDRESSEE RUPNS, DOANE, SWECKER & MATHIS STREET: 699 Prince St.
CITY: Alexandria
                                                                                                                                             128 AA
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE. 25.0AN-1995.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912 2007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/856,281 FILING DATE: 23-MAR-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/735,054 FILING DATE: 25-JUL-1991 ATTOPNEY/ASENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
IOR ADDITO: 1995
                                                                                                                                             PPT;
                                                                                                                                                                                                                                      Sequence 63, Application US/08478039 Patent No. 5681722 GENERAL INFORMATION:
                                                                                                                                                                                                                 Sequence 63, Application US/08478039.
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MEDIUM TYPE. Floppy disk
COMPUTER: IRM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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PECISTPATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INF/HMAIION FOR SEQ 1D NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: not relevant #OPOLOGY: not relevant
                                                                                                                                                                                                                                                                         APPLICANT: Newman, Poland A
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 amino acids
                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURPENT APPLICATION DATA
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                     2 VQLLEQSGAEVKKPGSSVKVSCQVFGDTFSPYTIQWLPQAPGQGPEWMGNIIFVYNTPNY 61
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                                                                  4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: William M. Smith
STREET: One Market Plaza, Stemart Towor, Smito 2000
                                      Scare 551; DB 7; Lenuth 128;
Fied No. 6.93e-34;
                                                                  9; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                             102 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEFERENCE/POCKET NUMBER: 14643-9-2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT/US92/10983
CHRUMUSCUME/SEGMENT: VH1 CONSENSUS
ACE 128 AA; 14138 MW; 114948 CN;
                                                                                                                                                                                                                                                                                                                                                                                Sequence 63, Application PC/THSG210983
GENEPAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-UOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                        Sequence 63, Application PC/Ins9210983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
JENCE 102 AA; 10940 MW; 55781 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30,223
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                                                                                                                                                                                                                                                                             STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 102 amino acids
AMINO ACID
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                                        59.2%
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California
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Bost Local Similarity 77.8%;
77, Conservative
                                                   Logal Similarity 63 3%;
les 81; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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               SEQUENCE
                                        Query Match
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AMINO ACID
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Local Similarity 77.8%;
es 77, Conservation
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US-07-834-539A-55
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Pred. No. 8.30e-34;
...matches 12: Indels 1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lonberg, Nils
APPLICANT: Kay Pobert M
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          One Market Plaza, Steuart Tower, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORPESPONDENCE ADDRESS: ADDRESSED: Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER. IBM PC compatible
OPERATING SYSTEM: PC-PoS/MS-POS
SOFTWARE: Patentin Pelease #1 0, Version #1 25
CURPENT APPLICATION DATA:
                                                                                                                                                                                          102 AA
                                               64 YAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCAR 102
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                                                                      14643-9-3
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APPLICATION NUMBER. IIS 07/940,860
FILING DATE: 16-DEC-1992
PRIOP APPLICATION DATA.
APPLICATION NUMBER. IIS 07/810,274
FILING DATE: 17-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/053,131
FILING DATE: 26-APP-1993
CLASSIFICATION: 800
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MOLECULE TYPE: protein
JENGE 102 AA; 10940 MW; 55781 CN;
                                                                                                                                                                                                                                                                                                                                                           Sequence 63, Application US/08053131
Patent No. 5660016
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
                                                                                                                                                                                                                                                                                                                                       Sequence 63, Application US/08053131
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415-326-2422
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                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Smith, William M. PEGISTRATION NUMBER: 30
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COMPUTER PEADABLE FORM:
MEDIUM IYPE: Floppy of
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STATE: California
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XX SEQUENCE 53, APPLICATOR PARENT INCOME

CC APPLICANT: Kay

CC APPLICANT: Kay

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5 QVQLV-QSGAEVKKPGSSSVKVSCKASGGTFSSYATSWVPQAPPGLSLEWMARTIPTLATAN 63
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Pred No. 8.30e-34;
9, Mismatches 12; Indels 1, Gaps
                                                                                                                                                                                                                                                                   APPLICANT: Lonberg, Nils
APPLICANT: Kay, Pobert M
TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMBUTER IBM PC COMBALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1 0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
FCT/::S92/06185
FILING DATE: 19910828
102 AA
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PRT;
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MOLECULE TYPE: peptide
JENCE 102 AA; 10940 KW; 55781 CN;
                                                                                                                                                          Sequence 55, Application PC/TUS9206185
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TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 14
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SEQUENCE CHAPACTERISTICS:
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NAME: Smith, William M.
PEGISTPATION NUMBER: 8765
STANDARD;
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STATE:
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APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5633425-Human Animals Capable of
TITLE OF INVENTION: Producing Heterologous Antibodies
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59.1%; Score 550; DB 7; Length 102;
Best Local Similarity 77.8%; Pred. No. 8.30e-34,
Matches 77; Conservative 9; Mismatches 12; Indels 1: Gaps
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GENERAL INFORMATION:
APPLICANT: Co. Man Sung
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: L. Selectin
NUPRES OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco
                                                                                              SSEE: William M. Smith
T. One Market Flaza, Steuart Tower, Suite 2000
San Francisco
: California
                                                                                                                                                                                     OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CUPPENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 YAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCAR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 YAQKFQGRLSITADDSTSTAYMELSSI.RSEDTAVFCAR 99
                                                                                                                                                                                                                APPLICATION NUMBER: US/07/834,539A FILING DATE: 19920205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application PC/TUS9311512.
                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
JENCE 102 AA; 10940 MW; 55781 CN;
          Sequence 55, Application US/07834539A Patent No. 5633425 GENERAL INFORMATION:
                                                                                                                                                                MEDIUM TYPE. Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 146
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEPHONE: 415-543-9643
INFORMATION FOR SEQ ID NO: 55:
                                                                                                                                                                                                                                                                 30,223
                                                                                                                                                                                                                                           ATTORNET/AGENT INFORMATION:
NAME: Smith, William M.
PEGISTPATION NUMBER: 30.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDAPD:
                                                                                                                                                                                                                                                                                                                                   : 102 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                          SEQUENCE CHAPACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                       single
                                                                              NUMBER OF SEQUENCES: 7'
                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                  94105
                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                        COUNTRY
                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                       CITY: S
STATE:
                                                                                                             STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1900
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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79 YNEKFKGRVIIISDESINTAYMELSSLRSEDIAVYYCAREEYGNYVR-----YFDVWGQG 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO CELL CYCLE-INDEPENDENT GLIOMA SURFACE ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 58.9%; Score 548; DB 11; Length 140; Local Similarity 65.4%; Pred. No. 1.19e-33; es 83; Conservative 17; Mismatches 21; Indels '
                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/HS94/1617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 2300 Richmond-Adelaide Centre
STREET: 101 Richmond Street West
                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                               11823-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
SEQUENCE 140 AA; 15650 MW; 117746 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08264093
Patent No. 5639863
GENERAL INFORMATION:
APPLICANT: Michael D. Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08264093.
                                                                 E. Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                              NAME: Smith, William M. REGISTRATION NUMBER. 30,223
                                                                                                                                                                                                                                                                                                                             PEFERENCE/FOOTKET NUMBER. 11. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ridout & Maybee
                                                                                                                                                                                                                                                                                                                                                                       415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                              140 amino acids
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      415-326-2422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: M5H 2J7
COMPUTER READABLE FORM:
                                                     COMPUTER READABLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                     CLASSIFICATION:
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                   USA
                                                                         MEDIUM TYPE.
                                                                                                                                                                                     FILING DATE:
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                                 94105
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                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                      1 EVQLLEGSGAEVKKPGSSVKVSGQVFGDTFSPYTIQWLFGAPGGGPEWMGNIIPVYNTPN 60
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TITLE OF INVENTION: Humanized Antibodies Peactive with
TITLE OF INVENTION: L'Selectin
UNBER OF SEQUENCES: 12
CORPESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIPEET TOWNSEND TOWNSEND Khourie and Grew SIPEET. One Market Plaza, Steuart Tower, Suite 2000 STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                        Length 121;
                                                                                                                                                                                                                                                                                            21, indels
 *MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: MS-DOS 5.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DGS/MS-DGS
SOFTWARP: PALEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/MS93/11612
                                                                  FILING DAIE:
CLASSIFICATION: 536
PILO APPLICATION: 536
ATTORNEY AGEN! INFORMATION:
NAME: Lake, James R.
REGISTATION NUMBER: 31081
REEPERPENDE/CONTEXT NUMBER: 31081
FEEDERONG TO THE TOWN NUMBER: 1000 PAIRS TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                      Score 546; DR 7; L
Pred. No. 1.71e-33;
                                                                                                                                                                                                                                                                                             17; Mismatches
                                                          08/08/264,093
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                                                                                                                                                                                                                                                 121 AA; 13281 MW; 86979 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application PC/TUS9311612.
                                                                                                                                                                                                                          not applicable
                                                                                                                                                         TELEPHONE: (416) 868-1482
TELEFAX: (416) 362-0823
INFORMATION FOR SED ID NO. 3.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                     LENGTH: 121 amino acids
TYPE: amino acid
STPANDEDNESS: not applic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDAPP
                                    SOFTWARE: ASCII Editor
CUPPENT APPLICATION DATA:
APPLICATION NUMBER: US/
                                                                                                                                                                                                                                                                      Match 58 6%;
Local Similarity 65.4%;
es 83; Conservative
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                                                                                                                                                                                                                                       linear
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CLASSIFICATION:
MEDIUM IYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVQLILEQSGAEVKKPGSSVKVSCQVFGDTFSRYTIQWLRQAPGQGPEWMGNIIPVYNTPN 60
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Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Haracid E.
IIII.E. OF INVENTION: HAPPGVED HUMANIZED IMMUNOSIOBLINS
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                 Score 545; DB 11; Length 121
Pred. No. 2.05e-33;
18; Mismatches 21; Indels
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ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Imbarcadero Center, 8th Floor CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 AA.
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
                                                                                                          11823-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPEPATING SYSTEM: PC-POS/MS-POS
                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
JENCE 121 AA; 13661 MW; 87993 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 104, Application US/08477728
                                                              NAME: Smith, William M.
PEGISTPATION NUMBER: 30,223
PEFERENCIONINGER: 1182
IELECOMMUNICATION INFORMATION:
TELECHONE: 415-326-2400
TELEFAX: 415-326-2422
                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STPANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDAPD:
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 64.6%;
Matches 82; Conservative
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US-08-477-728-104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1900
                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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US 07/590,274

APPLICATION NUMBER:

US-08-844-215-2.rai

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Ouery Match
Best Local Similarity 76 5%: Pred No 2 93e-33;
Matches 75; Conservative 11; Mismatches 11; Indels 1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CO, Man Sung
APPLICANT: SCHEELDER, William P.
APPLICANT: CANDOLET, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARF: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew STREET: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 YAQKFQGRVIITADESTNTAYMELSSLRSEDTAFYFCA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11823-002600
   FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 03 07/316,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,230,260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
JENCE 117 AA; 12472 MW; 77871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 72, Application US/08487200 Patent No. 5693762 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 72, Application US/08487200.
                                                                                                                                                                                                      TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2420
INFORMATION FOR SED ID NO: 104:
SEQUENCE CHAPACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
                                                                                                                                                                        REFERENCE/DOCKET NUMBER. 11.
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                              single
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STATE: California
                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1900
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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1 QVQLV-QSGAEVKKPGSSVKVSCKASGGTFSRSALIWVRQAPGQGLEWMGGIVFMFGPPN 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.3%; Score 543; DB 7; Length 117; 76.5%; Pred. No. 2.93e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 58.3%; Score 543; DB 7; Lendth 11/
Best Local Similarity 76.5%; Pred. No. 2.93c<sup>33</sup>; Matches 75; Conservative II; Mismatches 11; Indels Matches Asia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 YAQKFQGRVIITADESTNTAYMELSSLRSEDTAFYFCA 97
                                                                                                                                                                                                                                                                                                          11823-002610
                                                           PRIOR APPLICATION NUMBER: US U7/590,274
PRIOR DATE: 28-SEP-1990
PRIOR APPLICATION DATE: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATE: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY AGENT INFORMATION:
APPLICATION NUMBER: US 07/634,278 FILING DATE: 19-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY linear
MOLECULE TYPE: peptide
JENCE 117 AA: 12472 MW: 77871 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: Tue Feb 24 07:33:46 1998 Job time : 14 secs.
                                                                                                                                                                                                                                                                                                      PEFERENCETOCKET NUMBER: 11E
TELECOMMUNICATION INFORMATION:
TELEFHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                 NAME: Smith, William M
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                           117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEVUENCE
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recognize a region mapping at the carboxyl-terminal part of the HVRl Mereover, our results show that antibodies from all three samples samples while the ocquate viral sequence became predominant. the bloodstream; the reactivity increased in the second and third int estatosi faniv eft to eonameapqa ett ette viral etgener at the viral talator isolata assay (ELISA). We observed reactivity against this HVRI sequence in anadrosonummi beknil-emyzne yd seibodiina lo noitoeten iol napytana predominant in both the serond and third samples, was used as the amino acids, corresponding to the HVRL sequence found to be from three serum samples, collected during 18 months of follow-up, from an asymptomatic HCV-infected patient. A synthetic peptide of 27 sednesuced the hypervariable region 1 (HVF1) of the virus isolated mutation rate in crucial regions of the viral genome. We have becaraceuce is evasion of the host immune response through a high disease. A mechanism proposed as being responsible for virus The hepatitis C virus (HCV) is a frequent cause of chronic liver ЯA 60565T EW GENBYNK-X19611; GENBYNK-X19615; GENBYNK-X19613 SO Gancer Journals; Priority Fournals ΕS ruditsh AΊ Journal: Article; (JOURNAL ARTICLE) DI United States CX Cournal code: KdV. IsSM: 0082-538X. COURNAL OF VIROLOGY, (1995 Jul) 69 (7) 4407-12. OS PSOCACEIG (NCI) (CIAIN) 10083IA 089 (GIAIN) S8718IA NC Fome, Italy. Istituto di Ricerche di Biblogia Molecolare P. Angeletti (IRBM), SD D. IUOGEJL Scarselli E; Cerino A; Esposito G; Silini E; Mondelli M U; UA viremic hepatitis C virus-infected patients. briegine envelope glysoprotein (gp70) hypervariable region lin Occurrence of antibodies reactive with more than one variant of the $_{
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corresponding to the sequence derived from the patient described above and the second one synthesized according to the sequence of the HCV BK strain. A high frequency of positive reactions against both HVRI variants was detected in the samples from the viremic individuals. Finally, antibodies cross-reactive with both variants andividuals. Finally, ontibodies cross-reactive with both variants patients. The potential negative implications of this observation patients. The potential negative implications of this observation

nonviremed. Two synthetic peptides were used, the first

the same patient. The presence of anti-HVRI antibodies was investigated in a further 142 HOV patients: 121 viremit and 21

and are cross-reactive with the HVRL sequence previously found in

for the host are discussed.

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             to noitubedies the discussion of the resolution of the resolution of
         outside of HVRI dan indude Virus neutralizing antibodies, these
 cultures. The results suggested that although a few B-cell epitopes
               neutralize the binding of MCV to susceptible cells in tissue
                   against pEl and pE2 delts were tested for their ability to
were associated with resplution of infection. Rabbit antisera raised
       or chronic infection, whereas antibodies against protein po-HAVEL
   delta did not differ significantly between patients with resolving
E-cell epitopes. The antibody responses against profeins pEl and pE2
        uterior sufercipal edelevies VCH eAd to small esect teAd gains augment
          ed figure transportation of the description and street states and the results of the contract 
laver disease. A high prevalence of antibodies (up to 95.7%) against
 patiends who later mesolved an acute infection or developed chronic
               (HCV-AD78). Sees were obtained 4-3 months postinfection from
antibodies in sera of patients infected with the same isclate of HCV
              inmunoprecipitation assay to detect the presence of antiviral
                   expressed separately. These three proteins were used in an
          represents amino acids 684-410 of HVR1 of isolate HCV-AD78, was
             delta contained no HVRI. As a control, protein pG.HVRI, which
     411-688 of E2, respectively, of isolate HCV-AD78; the protein pE2
   in vitro translation. They represent aming acids 174-337 of El and
   hypothesis, two HCV protenns, pEl and pE2 delta, were generated by
               the induction of virus neutralizing antibodies. To test this
     ofher than the hypervariable region 1 (HVP1) might be involved in
     eunejobe broteins El and El sudgests that parts of these proteins
            (NOH) state of statishing the figure properties of they (NOH)
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                                                                Tournal code: KEA, ISSN: 0042-6822.
              Institut fur Virologie, Universitatsklinikum, Essen, Germany.
ViRology, (1998 Apr 10) 248 (2) 318-21.
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         recymer S; Rispeter K; Meisel H; Kraas W; Jung 3; Roggendorf M;
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             smark 5 signified gradied bacacad edopeda or pedcearg sempoquation
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viral neutralization.

Journal; Article; (Julynah ARTICLE)

Journal code: 8L7. ISSN: 0804-8508.

ARCHIVES OF VIROLOGY, 1997: 142 (3) 523-34.

Zibert A; Dudziak P; Schreier E; Roggendorf M

Institut fur Virologie, Universitatsklinikum Essen, Federal Republic

Characterization of antibody response to hepatitis C virus profein end significance of Appervantable region lespecific antibodies in

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creating own esent neemploot throughly different free mean the partent 17 of 28 partents (74) with chronic disease. The time of appearance ut pue sucribectat futfattuffes eange futfattuffestible sucribed (2): were found at least at one time point during the infection course in chronic infection ($n=\pm 1$) were studied. Antibodies directed to HVRL x = (8) = x) buttenfr felse soute soute x = x = x = xHCV-AD78. 307 sera obtained at different time points post infection peptide to detect antibodies against the main HVPI variant of offethers a prize bedatidatee asw (ASILE) Yasaa tredrozorummit besin:1-emyzne nA .(87GA-VOH) n:Ludolpoummi d-ifac besinimatico VDH a ic esalest emas edy the besteant need eval con asineitag tected to HVPl during the course of infection in a large group HCV isolate in vitro. We analyzed the appearance of antibodies virus (HCV) have recently been shown to neutralize the corresponding O standard to (187H) I motyem elfablarvaegy/A ou beddeath sembodionA 5070769I EM10155T ΕW ELICETEY Courrals EZ English AΠ dournal; Article; (JOURNAL ARTICLE) DL United States CX Jeurnal code: GBD: ISSN: 0270-9139. Institut fur Virologie, Universitätsklinikum Essen, Germany. HEPATOLOGY, (1997 May) 25 (5) 1245-9. os SD Incorp. A: Metat H: Krats W; Schulz A; Jung G; Roggendrafi UA istaty C sidideqed do sacidoelah pahdimul-11es edube daiw pagetiosse et l'upipa algerienzagne pagetien pagetien asuodsa Apoquin epagetien $_{\rm II}$ 87.798776 D11 WEDFINE 87398376 ИA AMSWEP 4 OF 18 MEDLINE ZП early p.i. dan neutralize virus of the anti-D 199 preparation. fibroblasts suggested that HVR1-specific antibodies in sera obtained and hot of VOH lo seibuds dramandests yd eres theited ni seiboditas in single patients. Further characterization of the HVFL-specific obtained early (< or = 1 year p.i.) and late (up to 14 years p.i.) Erres edf lo decoment bedoebeb ed bluco seibodidna bilibeqe-IAVH (198) preparation was studied. Using immunoprecipitation and ELISA, single-source outbreak by an HCV sontaminated anni-D immungliputin HVRL-specific antibodies in sera of patients who were infected in a suggested replication of HOV in these sells. The significance of stasidindii nsmud ic noideelni netis muluseni edi od bensqmos RCV. Occurrence of mutations in the nucleotide sequence of HVFL as to notizatilatruuq yauda od mekmo ni kedildatee aaw alleo taabloodii nemna is Yesse taithaid notteetair critin at nA .eurisetti estiteriuman viral glycoprotein E. of hepatitis C virus (HCV) are postulated to Antibodies directed against hypervariable region 1 (HVR1) within the ЯA t0108661 MΞ. T0866T EWPriority Journals; Canser Journals EZ

yidy (84 \pm) in this group for patients and most of the patients

groups (P · .025) although appearance and titers of other true droups (P · .025) atthough appearance and titers of other true droups deviate antibodies were found to be similar at early time HVV-specific antibodies were found to be similar as of all series (43%) of respective patients with serie available within the tirst 6 months p.i. were anti-HVRI positive. The highest prevalence of anti-HVRI in this group of patients was within month 6 to 12 p.i. (64%). None of this group of patients was within a such antibodies. In contrast, only 2 of 15 series (13%) of chronically infected patients with respective time points of series were anti-HVRI positive within worth 7 to 12 p.i. and only 5 of 18 series (28%) were pisting time points showed at least two consecutive anti-HVRI negative early time points showed at least two consecutive anti-HVRI negative early time points up to month 18 p.i. Prevalence of anti-HVRI after 24 months p.i. was up to month 18 p.i. Prevalence of anti-HVRI after 24 months p.i. was

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JOURNAL OF VIROLOGY, (1997 May) 71 (5) 4123-7. Institut fur Virologie, Universitatsklinikum Essen, Germany. Zibert A; Kraas W; Meisel H; Jung G; Roggendorf M I in acute self-limiting and chromic infections due to hepatitus C Epitope mapping of antibodies directed against hypervariable region 99181746 99585CL6 WEDFIKE MISMER 5 OF 15 MEDIUME vaccine development. implications for prognesss of the disease and also for any furure and yam bas seltesting in a self-limiting intestion and may have findings suggest clearance of virus by respective neutralization maintained high levels of anti-HVR1 for up to 17 years p.i. Cur

O end of bescenib Viniam era doing selboditana inebneqebni-etalosi (iii) bas VOH de saeireelai gaittmil-fles etues hitw betsioesss si IRVH To sunimast Whelf of beccease disposition to (notice) interesting of (HCA). Our results suggest that (1) an early appearance (up to month

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and reflexantering refired the colline and the reflexantering the section of T remminus of HVRL seem to persist in chronically infected parients.

all of whom were infected with the same aclate of whom mere in the entryme-fluked immunosorbent assay varist follow-up sasa in partents.

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evaluated by characterication of a rabbit serum.

Epitopes of hypervariable region 1 (HVP1) were mapped by

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Institute of Virology, University of Essen, Germany. SO

VIROLOGY, (1995 Apr 20) 208 (2) 653-61. OS

Journal code: XEA. ISSN: 0042-6822.

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variants of HVR1 were found in sera obtained early postinfection absolutely isolate-specific. Antibodies directed against individual extent (15%), suggesting that not all HVR1-specific antibodies are rassel a of tid A.18VH beingoter osia Maerdiuo ed to moitbelini perdent of sera contained antibodies to HVRLA. Sera unrelated to -ualler- Λ ixis into projection $ext{gradient}$ at superpad uotsny se pesseadhe determined. The four malor variants (HVR1.A, B, C, and D) were with a full sequences of ability matter in the FAC Market with the sequences and severe with the sequences of the sequences o edT .(87CA-VDH) noideragerg miludolpennumi C-idna bedanimatnes e Kq yeeaqance extresequis e ut peoceau extended anticed po exes C virus (HCV) can neutralize virus. We studied such antibodies in region I (HVEI) within the putative envelop protein E2 of hepatitis eld has been postiled the tanificales specific to the hypervariable.

later. An in vitro binding assay of HCV to tissue culture cells was

(p.i.) (< or = 1 year) but also in sera obtained several years

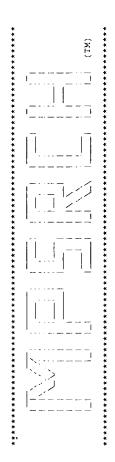
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employed to further characterize these sera. Five of seven sera that were obtained early p.i. prevented binding of HCV to cells. Preincubation of such sera with HVRL-specific fusion proteins restored binding of HCV to cells in four of five sera. These findings suggest that the majority of neutralizing antibodies are directed against HVRL.

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US-08-844-215-16.rng

Page 1



Pelease 2 12 John F. Gollins, Biocomputing Pesearch Unit Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntolliGenetics, Inc.

n.a. - n.a. database search, using Smith Waterman algorithm MPsrch_nn Maspar tire 50 99 Seconds 706.142 Million cell updates/sec TOB FEE 24 07 72 45 1999 Fun on

Tabular output not generated.

(1-312) from USC8844215.seq 312 >US-08-844-215-16 Description. Perfect Score: Title:

GGACCAAGGTGGAGATCAAA 312 COTGGTTCCACCTCTAGTTT CTCCASCTGACTCACACCTCC 1 SASCICACICASICIOCAGO N.A Sequence

TABLE default Gap 6 Scoring table.

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Listing first 45 summaries Minimum Match 0% Post-processing:

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Mean 8.010; Variance 4.828; scale 1.659 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

	Pred No	VK65.3, 9.256-258	V. Adppd gene VK 9.256-158 DNA fragment VK 9.256-158	V-kappa gene vk 1.46H-153	1 1	VK55.5, 1.460-153	light chain varia 5.71e-148	IgG aberrant ligh 5.71e-148	onas aeru 1.36e-139	1.366-	ssion vec 3.38e-138	3,39€.	toxoid 1 8.38e-137	i-tetanus 8.38e-137	ing human 2.08e-135
ņ	Description	ENA fragment vk65.3,	Human P.A. fragment	Ношап V-Карр	Human DNA fragment vk	DNA fragment Vk55.5,	IgG light ch	1Bl IgG aber	Anti-pseudomonas aeru	Anti-P. aeruginosa st	pComb3 expression vec	Expression vector,	Anti-tetanus toxoid l	pC3AF313 anti-tetanus	Sequence coding human
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ALIGNMENTS

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Example 21. Fig 41, 34pp, English.
The present sequence is the variable kappa chain gene segment the present sequence is the variable kappa chain gene segment occitaining human DNA fragment, vk65.3, which was co-injected along with the human DNA fragments vk65.5, vk65.8 and vk65.15 into half day mouse embryo pronuclei, to generate an unrearranged light chain minilocus transgene. The resulting transgenic mice can be used for the production of heterologus (i.e. human) antibodies against specific antigens, this comprises immunising a mouse with a human gamma immunoglobulins.
                                                                                                              14-APR-1997 (first entry)

DNA fragment vk65.3, containing variable kappa chain gene.

Variable: kappa chain; gene segment; human; DNA fragment; vk65.3;

unrearranged, light chain; minilocus; transgene, transgenic; mouse;

Production, heterologous; antibody; gamma, immunoglobulin, ss.

Homo sapiens.
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T37180 standard; DNA; 812 BP.
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17-DEC-1991; US-810279;
18-MAR-1992; US-853408;
23-JUN-1992; US-990068;
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(GENP-) GENNHARM INT INC.
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P-PSDB; W03946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig. 41: 296pp; English.
Human DNA fragments vk65.3, vk65.8 and vk65.15 (given in Human DNA fragments vk65.3, vk65.8 and vk65.15 (given in U78852-078955, respectively) each contain a V-kappa acme seament that can be used to form a complete human light chain minilocus transgene for expression in a nonhuman transgenic animal for the veryous antibody production. The deduced amino acid sequences of the V-kappa coding regions are given in R6728-R62931. Sequence 812.8P.
                                                        Gaps
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                           Length 812;
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Human V-kappa gene vk65.3.
Transgenic mouse, transgenic animal; antibudy engineering; variable region; light chain; minilocus transgene, chimeric antibody; ss.
190 T:
187 G;
                                          Pred. No. 9.25e-158;
                             DB 27;
                                                        Mismatches
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    812 BF;
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502 gecagicagagigitageagetaetiageeiggiaeeaaeagaaaeeiqgeeaggeieee 561
                                                                                                                         67. GCCAGTCAGAGTGTTAACAAGTACTTAGCCTGSTAYCAAYAGAAAY 1.00CAGCTGGGTAGCT.
                                                                                                                                                                    562 aggetecteatetatgatgeatecaacagggeeactggeateceagecaaqtteaatggr 621
                                                                                                                                                                                   622 agtgggtetgggaeagaetteaeteteaeeateageageetagageetgaagatttgea 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                became to the specific oligonic location of 50327 was used to probe a human placental genomic DNA illeary clowed into lambane MRIS, ST., T. DNA Iragments from Fostil's Flair Clones were subcloned into plasmid vectors. Variable genomics selected on the basis of open reading transes, intext dones were selected on the basis of open reading transes, intext donor and seceptor splice sites and intact recombination sequences. The sequences obtained from four different plasmid clones were
              S, Japs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transgenic non-human animals contg. immunoglobulin heavy chain trans gene - used to produce useful antibodics by isotype
                                                                                                                                                                                                                                                                                                                                                                                                                          10.NOV-1993 (first entry)

Human DNA fragment vk65.3 containing V-kappa gene segment.

Humanoglobulin: light chain variabie region, minilocus;

isotype switching; unrearranged functional Vk gene segment:
human light chain transgene; ss.
                6, Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note "splicing and recombination signal sequences"
Pred. No. 9.25e-158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             initiation codon, i.e. the start of the ORF;
the precise start point of the exon is not
indicated"
                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /number= 2
/note= "ORF not terminated by a stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /number= 1
/note= "nucleotides 199-201 represent the
                                                                                                                                                                                                                                                                                                 682 gtttattactgtcagcagcgtagcaactgg 711
                                                                                                                                                                                                                                                                                                                             247 GITIATTACTGTCAGCAGGGTAGGTAGTTGG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 21; Fig 41; 196pp; English.
                   .;
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                                                                                                                                                                                                                                                                                                                                                                                               Q44222 standard: DNA: R12 BP.
 Best Local Similarity 97.8%;
Matches 264; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUN-1992; US-904068.
(GENP-) GENPHARM INT INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          419..714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-DEC-1991; US-81U279.
18-MAR-1992; US-853408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T10983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lonberg N:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93-214169/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; R38648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 - JUN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intron
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442 acacagtotocagecaceetgtetttgtetecaggggaaagagecaceeteteetgeagg 501
                                                                                                                                                                                                        502 gocaqtcaqaqtgttagcagotacttagootggtaccaacagaaacotggocaggotcoc 561
                                                                                                                                                                                                                                      67 GCCASTCAGAGTGTTAACAAGTACTTAGCCIGGTACCAACAAGAAGCTGGCCAGGCTCCC 126
                                                                                                                                                                                                                                                                        562 aggetecteatetatgatgeatecaacagggecaetggeateceagecaggtteagtgge 621
                                                                                                                                                                                                                                                                                                                                         622 agtgggtotgggacagacttcactotcaccatcagcagcctagagcctgaagattttgca 681
                                                                                                                                                                    7 ACTCAGICICCAGCCACCTGICTTTGICICAGGGGAAAGAGCCACCCTCTCCTGCAGG 66
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure: Fig. 42: 296pp. English
Human DNA fragments vk65 3 vk65.5. vk65 9 and vk65.15 (given in
Human DNA fragments vk65 3 vk65.5. vk65 9 and vk65.15 (given in
Human DNA fragments vk65 3 vk65.5. vk65 9 and vk65.15 (given in
that can be used to form a complete human light chain minilocus
transgene for expression in a nonhuman transgenic animal for
heterologous antibody problection. The deduced amino asid
sequence of the V-kappa coding regions 104 0:
Sequence 200 HP. Vappa coding regions 104 0:
207 TE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transgenic non-human animals producing heterologous or chimeric antibodies [ ] for binding a pre-determined human antigen with
designated_p65.3, p65.5, p65.8 and p65 15 (son 244222-244225,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-30W-1995 (first entry)
Human V-kappa gene vk65.5.
Hransgenic mouse; transgenic animal; antibody engineering;
Variable region; light chain; minilocus transgene;
chimeric antibody; ss.
                                   Match 82.7%; Score 258, DB 7, Length 812, Local Similarity 97.69, Fred. We 9.25e-178, tes 264; Conservative 0; Mismatches 6; Indels
                                   187 0:
                                                                                                                                                                                                                                                                                                                                                                                                         682 gittattacigicagcagcgiagcaacigg 711
                                                                                                                                                                                                                                                                                                                                                                                                                                         247 GITTAITACTGICAGCAAGGGAGGGACTGG 276
                                   378 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                   201 A;
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Q78953 standard; DNA; 900 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-APR-1994; UG-580.
26-APR-1993; US-053131.
22-JUJ-1993; US-096762.
18-NOV-1993; US-155301.
03-PFC-1993; US-16739.
10-DEC-1993; US-165699
09-MAR-1994; US-165699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Splicing_signal
                                   812 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     increased affinity
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                 respectively
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                                   Sequence
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                                                                     Query Match
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                                                                                                                           481 gecagicagggigitagcagetaettageeiggiaecageagaaaeeiggeeaggeieee 540
                                                                                                                                                       57 SCCASTCAGASTSTIAACAASTATITAGGGGTGTGGTAGAGAAACGTGGGCGAGGGTGCC 126
                                                                                                                                                                                      541 aggeteeteatetatgatgeateeaaeagggeeaetggeatereageraggiteagiggr 600
                                                                                                                                                                                                                                                  601 agigggeotigggacagaetteaeteteaecateageageetagaggeetgaagatttigea 660
                                                                                                                                                                                                                                                                                187 AGIGGOLGIGGGAGAGAGIICAGICICACCAICAGGAAGCIAGAGCIGAAGAIGIIGCA 246
                                  Sdes
                                                                                            7 ACTOAGLOTOCAGOCACOCTSTCTLIGTCTCCAGGGGAAAGAGCCACCCTCTCCCTGCAGG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 21, Fig 42, 196pp, English.

The V-kappa specific of group neartish of an as used to prake a human placental genomic ENA library cloned into lambdaEMEL/SPS/T7.

ENA fragments containing V-kappa segments from positive plage clones were subcloned into plasmid vectors. Variable gene segments
                                                                                                                                                                                                        Transgenic non-human animals contq. immunoglobulin heavy chain trans gene — used to produce useful antibodies by isetype
                                  Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human DNA fragment vk65.5 containing V-kappa gene segment. Human DNA fragment vk65.5 containing V-kappa gene segment. Immunoglobulin; light chain variable region, minlivous, isotype switching; unrearranged functional Vk gene segment; human light chain transgene; ss.
 Length 900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "splicing and recombination signal sequence"
exon
                                Ġ
 Score 252; PB 12; Pred, No. 1.46e-153;
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/note= "nucleotides 180-182 represent the
initiation codon, i.e. the start of the ORF;
the precise start point of the exon is not
indicated"
                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag- a
/note= "splicing and recombination signal ?"
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/note= "OPP not terminated by a stop codon"
                                                                                                                                                                                                                                                                                                              661 gtttattactgtcagcagcgtagcaactgg 690
                                                                                                                                                                                                                                                                                                                                            247 GITIALTACTGICAGCAGGGIAGCGACIGG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
119..126
                                                                                                                                                                                                                                                                                                                                                                                           T
Q44223 standard; DNA; 900 BP.
T Match
Local Similarity of 78;
                                251; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229..397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUN-1993.
7-DEC-1992; U10983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PA, Lonberg N; 93-214169/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB: R38649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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 Guery Match
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421 acacagteteragecaccetgtetttgteteceaggggaaagagecacceteteetgeagg 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 GCCAGTCAGAGTGTTAACAAGTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 541 aggetecteatetatgatgeatecaacagggecaetggeateceagecaggtteagtgge 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  601 agigggcctgggacagacttcactctcaccatcagcagcctagagcctgaagattttgca 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the variable kappa chain gene segment containing human DNA fragment, va65.5, which was co-injected along with the human DNA fragments va65.3, va65.8 and va65.15 into half day mouse embryo pronuclei, to generate an unrearranged light chain minilocus transgene. The resulting transgenic mice can be used for the production of heterologous (i.e. human) antibodies against specific antigens, this comprises immunising a mouse with a preselected antigen and collecting antigen binding heterologous Sequence 900 BF; 225 A; 244 C; 204 G; 227 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                        7 Acteacretical desectater treferences and analysis of Acteacretical desectation of the Acteacretical and Acteacretical 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-ApR-1997 (first entry)

DNA fragment vk65.5, containing variable kappa chain gene.

DNA fragment; kappa chain; yene segment; human; DNA fragment; vk65.5;

unrearranged; light chain; minilocus; transgene; transgenic; mouse; production; heterologous; antibody; gamma; immunoglobulin; ss.
from the resulting clones were sequenced and functional clones were selected on the basis of open reading frames, intact donor and acceptor splice sites and intact recombination sequences. The sequences obtained from four different plasmid clones were designated p55.3, p65.5, p65.8 and p65.15 (see Q44222-Q44225,
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prodn. of heterologous human immunoglobulin(s) - by immunising
                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                   227 T.
                                                                                                                                                                                                                                                           Length 900:
                                                                                                                                                                                                                                                                                                                       9. Indels
                                                                                                                                                                                                      204 G:
                                                                                                                                                                                                                                                     Ouery Match

Best Local Similarity 96.7%; Pred. No. 1.46e-153;
Matches 261; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         661 gtttattactgtcagcagcgtagcaactgg 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 GITTATTACTGTCAGCGTAGCGACTGG 275
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                                                                                                                                                                                                          225 A.
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US-575962.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96-383736/38.
                                                                                                                                                                                                             900 BP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transgenic mice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-AUG-1990; U
17-DEC-1991; U
18-MAR-1992; U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5545806-A.
                                                                                                                                                                                  respectively)
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                                                                                                                                                                                                                    Seguence
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                                                                                                                                                                                                                           0; Caps
                                                                                                                                           Indels 0; Gaps
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The leader peptide and the L'V region are encoded in different reading frames. The L'V region corresponds to the last three amino acids of the leader peptide and the rearranged VJ gene. Clone 489-VkI5 (see Q11878) encodes an aberrant light chain containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 91-163947/22.
P-PSDB, P.12129, P12130, P12131.
Oligomeric immunoglobulin(s) with high avidity for antiqen(s) tormed by duplicating esp. variable region of light chain of Idd
                                                                                                                                     1gG light chain variable region clone.
1mmunoglobulin G, light chain; variable region; duplication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 C; 290 G; 402 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2: Length 1204:
           Length 900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Y Match 80.8%, 30500 252: PN 27; 1 Local Similarity 96.7%; Pred. No. 1.46e-153: hes 261; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= L'V region
/note= "translates from different reading frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            passivé immunity, group B streptococci; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    661 gtttattactgtcagcagcgtagcaactgg 690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q11879 standard; DNA; 1204 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BRIM ) BRISTOL-MYERS SOUIB. Shuford WW, Harris LJ, Raff
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See also Q11880.
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06-NOV-1990, U06425.
07-NOV-1989; US-4327
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                          Query Match
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                                                                             Matches
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71 acacagteteccagecaccetgtetttgteteccaggggaaagagecacceteteetgeagg 130
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            67 GCCASICAGAGIGIIAACAAGIACIIAGCCIGGIACCAACAGAAAGCIGGCGAGGCTGC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence encodes an aberrant light chain containing two L'V regions Antibody molecules of the invention can include one or two such aberrant light chains to produce heavier antibodies. These with just a single copy of the L'V region The clone is not complete; it starts with the G of the AIG initiator codon See also 01879 and 01887, 382 C; 302 G; 266 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 ACTCAGTCTCCAGCCAGCCTGTCTTTGTCTCCAGGGGAAAGAGCCATCCTGTGCAGG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligomeric immunoglobulin(s) with high avidity for antigen(s) formed by duplicating esp. variable region of light chain of \rm IgG
                                                                                                                                                                                                                                           1B1 IgG aberrant light chain clone 4B9/Vk15.
immunoglobulin G; light chain variable region; duplication;
passive immunity; group B streptococci; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 78.2%; Score 244; DB 2; Length 1242; Local Similarity 95.2%; Fred. No. 5.71e-149; hes 257; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                       /label* L'V l
/note= "encodes last 3 amino acids of leader and
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/label= L'V 2
/note= "encodes last 3 amino acids of leader and
                                                                                                                                          247 STITATIACIGICACCAGCGIAGCGACTGG 276
                                                                                                                931 gtttattactgtcaacaccgtgacaattgg 960
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Shuford WW, Harris LJ, Raff HV:
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Q11878 standard; cDNA: 1242 BP.
Q11878;
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/*tag= d
/note="constant region"
/note="constant region"
                                                                                                                                                                                                                               (first entry)
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06-NOV-1990; U06426.
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/note= "leader"
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P-PSDB; R12128.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     misc RNA
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P-PSDB; P81246, P81245.

P-PSDB; P81246, P81245.

Actil:Festadomenas aeruginosa type antibody L-chain coding DNA -
contains constant kappa and lambda type regions, and versatile
region recognising paseruginosa F4 and H1 types
Disclosure; Pages 610-511: 12pp; Japanese.

It also codes for a variable region recognising Ps.aeruginosa F4 and H1
types. The Ab can be used for immunologic control of infection caused by
Ps.aeruginosa. The antibody is made effective against various classes or
subclasses of registant Ps.aeruginosa by recombining corresp DNA L-chain
584 acgcagtetecaggcaccetgtet+tgt-ter-teragggggaagagcaccetetecagg 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              644 gocagicagagigitagcagcaaitectiageciggiaenaanagaaanciggnnaggn 703
                                                          251 agigggirigggaragacticanthiannatoagoagoctagagootgaagattitgoa 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 ACTICACTOTOCAGOCACCOTGTOTITGTOTOCAGGGGAAAGAGCCAGCCTGTGCTGCAGG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.4%, Soure 232, DB 2, Length 1911,
90 0%, Pred No. 1 36e-139,
Jailve 9, Mismatches 28, Indels 3: Gaps
                                                                                                                                                                                                                                             Anti-pseudomonas aeruginosa human type antibody L-chain coding DNA contg constant region of kappa and lambda types Pseudomonas aeruginosa F4; Pseudomonas aeruginosa H1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 G:
                                                                                                                    311 gtttattactgtcaacaccgtgacaattgg 340
                                                                                                                                              247 GTTTATTAGTGTGAGGGGTAGGGAGTGG 275
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                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Sequence 1011 BP, 237 A,
                                                                                                                                                                                                     N81637 standard; DNA; 1011 BP
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(WAKU-) Wakunaga Seiyaku KK.
                                                                                                                                                                                                                                  07-JAN-1991 (first entry)
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Rest Local Similarity
Matches 278; Conserv
                                                                                                                                                                                                                                                                                           immunotherapy; ss.
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/note="Claimed SQ"
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/note="P81247"
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                                                                                                                                                                                                                                                                                                                                       [ATA_signal
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/note="L"
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                                                                                                                                                                                                                   N81637;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 decadrocorcitordacadanticacitorancancancanciadadecidadantiti 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           production of human IgG monoclonal antibody - by converting human antibody into other subclasses by genetic engineering antibody into other subclasses by genetic engineering pisclosure; fig. 3: 17pp; Japanese.

Disclosure: fig. 3: 17pp; Japanese.

This encodes a variable chain and can be connected to a gene encoding a constant region which determines optional IgG subclass. This can be used to study subclasses, and as an antigen for prepg. IgGl or IgG3 antibody. Regions 325-372 connected to 560-571 encode the L chain, region 572-856 encodes V chain and region 857-895 encodes J chain. Sequence 1011 BP; 237 A; 263 C; 254 G; 257 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              584 acgcagictccaggcaccetgictitgictccagggggaagagccaccctctcctgcagg 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 644 gecagicagagigitageageaaticetiageetiggiaeeaaaaaaaetiggeeagget 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    704 cccaggotoctcatetatgetgegtecageagggecaetggeatereagaeaggtteagt 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 232; DB 1; Length 1011;
Pred. No. 1.36e-139;
0; Mismatches 28; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 ACTORGICICORRECACECTETITIGICICEARAGARAGAGCACCTETICETGCAGG 66
                                                                                                                                                                         824 gcagigiattacigicagcagiacgacgccigaicactiicggcggagggaccaagiig 883
                                 704 eccaggetecteatetatgetgegtecageagggeeactggeateceagacaggtteagt 763
                                                    ggcagtgggtctgggggagacttcactctaccatcagtagactggaacctgaagattct 823
                                                                                                                                     184 GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAACCTAGAGCTGAAGATTTT 243
                                                                                                                                                                                          67 GCCAGICAGAGIGIIA--A-CAAGIACIIAGCCIGGIACCAACAGAAACCIGGCCAGGCI 123
                                                                                                                                                                                                                                                                                                                                                                             02-MAR-1990 (first entry)
Anti-P. aeruginosa strain F4 light chain V and J coding regions
Immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
325..372
                                                                                                                                                                                                                                                                                                                                                          N91359 standard; DNA; 1011 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (WAKU) Wakumaga Seiyaku KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas aeruginosa F4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 560..895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-FEB-1988; 035395.
19-FEB-1988; JP-035395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89-303485/42.
                                                                                                                                                                                                                                                      884 gacatcaaa 892
                                                                                                                                                                                                                                                                                        304 GAGATCAAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= c
J01211498-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
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This sequence represents the prombs phagemid expression vector. This vector has been designed to allow for anchoring of expressed proteins on vector has been designed to allow for anchoring of expressed proteins on the bacteriophage coat protein, for an order in the afor residue minor phage coat protein, cpill (cp3), which is expressed prior to extrusion in the phage assembly process on a bacterial membrane and accumulates on the inner membrane lacoung into the periplism of E. conf. This plasmid was used within the scope of the invention to express various mutagenised human Fab's which comprise heavy and lish variable regions which bind to HIV qp120, pcombs allows for both surface display regions which bind to HIV qp120. pcombs allows for both surface display of combinatorial Fab ilbraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of combinatorial Fab libraries. Dicomo consists of a JNA mojecule having of combinatorial Fab libraries. Dicomo consists of a JNA mojecule having two cassettes to express one fusion protein, Fd/Kp3, and one soluble protein, the light chain. The finished vector comprises, operatively protein, the light cassette consisting of lacz promoter/operator linked 5 to 3' to 4 first cassette consisting of lacz promoter/operator sequences, a Notl restriction site, a ribosome binding site (RHS), a sequence, a spacer region, a cloning region bordered by 5' Mhol and pacteriophage cp3 followed by a stop codon, a Nhel restriction site between the two cassettes, and a second lacz promoter/operator sequence, between the two cassettes, and a second lacz promoter/operator sequence, between the two cassettes, and a second lacz promoter/operator sequence, clollowed by an expression control RBS, a PelB leader, a spacer region, a followed by expression control stop sequences and a second Not!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the MT4 Fab display phagemid expression vector, pMT4-3 (see also 092540), used in the invention for the production of synthetic human Fab antibodies against 9pl20 of HIV.
Sequence 4691 BP; 1170 A; 1171 C, 1232 C; 1118 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2677 gageteaegeagteteeaggeaceetgtetttgteteeaggqqaaagaqeeeeeretetee 2736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2737 igcagggccagicacagigitagcagggcciacitagccigqiuccagcagaaacciqqc 2796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TOCAGOGGGAGTCASAGTGTTASCAAG---TACTTAGGCTGGTACCAACAGAAACCTGGC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GABELTGACTGAGTGTGGAGGGGGGTGTTTGTGTGTGAGAGAAAGAGGGAGGTGTGTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 230; DB 16; Length 4691;
Pred. No. 3.38e-138;
0; Mismatches 32; indels 4; Gaps
                                                                                                                                                                                                                                            Gene III: flamentous phage; minor phage cost protein; opil; opis; bacterial membrane; periplasm; E. coli; human; Fab, HIV, 4pl20; combinatorial Fab library; cassette; Fd/cp3; lacz promoter/operator; ribosome binding site; RBS; PelB leader; spacer; tether sequence; MT4; pMT4-3; antibody; ss; cyclic.
                                                                                                                                                                                                                               pcomb3; phagemid expression vector; bacteriophage; coat protein 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunodeficiency virus - used for diagnosis and immuno:therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic human neutralising monoclonal antibodies to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 185-188; 249pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lerner RA;
                                                                                                                                          Q92546 standard; DNA; 4691 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-001-1993; US-139409.
26-APR-1994; US-233619.
19-SEP-1994; US-308841.
(SCRI ) SCRIPPS RES INST.
Barbas CF, Burton DR, Le.
                                                                                                                                                                                            11-MAR-1996 (first entry)
                                                                                                                                                                                                                       pcomb3 expression vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIV-induced disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-OCT-1994; U11907.
884 gacatcaaa 892
                                          304 GAGATCAAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95-170235/22
                                                                                                                                                                                                                                                                                                                                                                                                                    W09511317-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         27-APR-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the expression vector, poho-TT which is a modified version of the phagemid expression vector, pcomb3 given in (92546. pphr-TT provides for the expression vector, pcomb3 given in (92546. pphr-TT provides for the expression vector, pcomb1e Fabs which are secreted into the periplasmic space which is regulated from the alkaline to phosphatase (phoA) promoter. This plasmid was used within the scope of the invention to express various mutagenised human Fab's which comprise the variable regions which bind to HIV gpl20. psho-TI consists of a DNA molecule having two cassettes to express two soluble consists of a DNA molecule having two cassettes to express two soluble consists of a DNA molecule having two cassettes to express two soluble consists of a DNA molecule having two cassettes consisting of the phoA concert/operator sequences, an Enski restriction site, a ritosomm of region brondered by S. sact and Y. Xbal restriction for sites, an Nool restriction site between the two cassettes, and a second cassette consisting of an expression control stop sequences and a Notle sequence and a Notle sequences and a Notle statiction site. Asperer region control stop sequences and a Notle castiction site, and a second consisting of an expression control stop sequences and a Notle sequences and a Notle sequences of the phage of the province of the nucleotide sequences of the heavy and light chain stuffer that is 1200 by in length and a heavy cantable domains of a remain to the consistion of a person of the chains of a point of the nucleotide sequences of the heavy and light chain variable domains of a consistion of the consistion of the control of the control of a person of the control of
                                                               2857 ttoagtagoagtagatetaggacagaetteaeteteaetetususususususususettiili 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 1916 | 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4507 gageteaegeagteteeaggeaecetgtetttgteteeaggggaaagageeaecetetee 4666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4667 tgcagggcraqtcacagtgttagcagggcctacttagcctggtaccagcagaaacctggc 4726
                                                                                                                                                                                                 Ti-MAR-1996 (first entry)

Expression vector, pPho-TT.

Human, Fab, variable chain, heavy, light; region; VH, VL, HIV, gp120; 3b1; 3b3; 3b4; 3b9; MT4; humanised: monoclonal antibody; MAb; limmunoreaction: neutralisation; passive immunotherapy; tetanus toxin; alkaling phosphatase, phoA, Ss, cyclic
118 CAGGCTGCGAGGCTGCTGATGTATGATGCATGCAAGAGGGGGAGAGGAGAAGAGAGGAAGA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAGCICACICAGICICCAGCCACCITGICITIGICICCAGGGGAAAGAGCCACCCICTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic human neutralising monoclonal antibodies to human immunodeficiency virus (used for diagnosis and immunotherapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 6166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1629 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 73.7%; Score 230; DB 16; L. Best Local Similarity 88.9%, Fred. No. 3.38e-138; Matches 280; Conservative 0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1705 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Fage 193-197; 249pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burton DR, Lerner RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tetanus toxin-specific Fab.
Sequence 6155 BP; 1416 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T 12
Q92547 standard; DNA; 6166 BF.
                                                                                                                                                                                                                                                                                                                                       2977 aaggtggaactcaaa 2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-APR-1994; US-233619.
19-SEP-1994; US-308841.
(SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                       299 AAGGTGGAGATTAAA 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-0CT-1993; US-139409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV-induced disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-OCT-1994; Ullan7
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diversity antibody libraries, for screening antigens
claim 21; Page 84-85; 120pp; English
This sequence represents the light chain coding sequence derived from
This sequence represents the light chain coding sequence derived from
the surface display phagement of the coding sequence derived from
the surface display phagement and heavy and light chain variable
contains the bacteriophage gene III and heavy and light chain variable
domains sequences for encoding human feab antibodies against teranus toxin.
This sequence was pref. used in the method of the invention for the
production of antibody libraries containing increased diversity. The
sequences given in 470480-86 are primers which were used for inducing
mutagenesis in a complementary determining region (CDR) of an
immunoglobulin light chain gene. These primers contain a 3' terminus
capable of hybridising to a irst framework region and a nucleotide
sequence between the 5' and 3' termini having the forming (NNF),
when the CDF regions of immunoglobulins heavy or light chains that
the libraries with increased antibody diversity by inducing mutagenesis
are displayed an the surface of immunoglobulins heavy or light chains that
the library These primers of immunoglobulins heavy or light chain CDR3.

The libraries with increased antibody diversity by inducing mutagenesis
are displayed an the surface of immunoglobulins heavy or light chain CDR3.

The libraries with increased antibody mutagenesis
and libraries with increased antibody diversity by inducing mutagenesis
and displayed an the surface of immunoglobulins heavy or light chain CDR3.

Sequence 645 BP; 18C A; 197 C; 170 G; 127 T;
                                                                                W.04-APR-1995 (first entry)
Anti-terauss toxoid light chain cDNA from vector, pc3AP313.
Polymerase chain reaction: primer; mutagenesis; PCR: amplify,
diversity, antibody; complementatity determining region; CDR;
framework; constant; light; heavy; phage; immunoglobulin; library; ss.
                                                                                                                                                                                                                                                                   4797 tipayigspagtygythiggyahaganitbacipinancathaydaganiygaghrigaa 4846
                                                                                                                                                                                                                                                                                                                                                                                                                                                      4847 gatitigcagigiaciaciacigicagcagialggiggcicaccgiggiticggccaagggacc 4906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 caggirtorraggirtortortorigitadatecagoagggeoactggeateceagacagg 180
61 INCASSOCIANTOAGAGIGIIAACAAS---IACIIAGOTIGGIACCAAQAAAACIGGC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 tgragggcragtcacagtgttagcagggcctacttagcctggtaccagcagaaacctggc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 gageteaegeagteteeaggeaecetgtetttgteteeeaggggaaaggageeaeeetetee 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAGCTCACTCAGTCTCCAGCCACCTGTCTTTGTCTCCAGGGGAAA3AGCCACCCTCLCC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligo-nucleotides - used as PCR primers for producing increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.38e-137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match (3.1%; Score 228; DB 12; Bost Local Similarity 88.6%; Pred. No. 8.38e-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burton DR, Lerner RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-FEB-1994; U01234.
02-FEB-1993; US-012566.
28-DEC-1993; US-174674.
SCPI ) SPRIPPS PES INST.
Barbas CF, Burton DR, Ler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4907 aaggtggaactcaaa 4921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 caggeteceaggetecteatetatggtacatecageagggeeactggeateceagaeagg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 tecagtggeagtgggtetgggaeagaetteaeteteaceateageagaetggageetgaa 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 TICAGISGCAGIGGGTTTGAGAGAGTTCACTGTCACCATCAGCAACTAGAGGTGAA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1: Page 84: 125pp: Enalish Example 1 Page 84: 125pp: Enalish Introduction 1 Page 84: 125pp: Enalish Introduction 1 Page 84: 125pp: Enalish Introduction 1 Page 84: 125pp: Enalish Internation 1 Page 84: 125pp: Enalish Introduction 1 Page 84: 125pp: Enalish Introduction 1 Page 1 Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 tgcagggccagtcacagtgttagcagggcctacttagcctggtaccagcagaaacctggc 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 gageteaegeagteteeaggeaeeetgtetttgteteeaggggaaagageeaeeetetee 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 33; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33-0CT-1996 (first entry)
pC3Ap313 anti-tetanus toxoid Ig light chain variable domain cDNA.
pC3Ap313 anti-tetanus toxoid Ig light chain variable; CDR:
Mutagenesis; Ig; immunoglobulin; FR; framework region; variable; CDR:
complementarity determining region; light; heavy chain; PCR;
polymerase chain reaction; antibody library; diversity; affinity;
immunospecificity; ss.
                                                                                                                               241 gattttgcagtgtactactgtcagcagtatggtggctcaccgtggttcggccaagggacc 300
                                                                                                                                                                                   238 GATTITGCAGITIATIACIGICAGCGIAGCGACIGGGICACTITCGGCGGAGGGACC 297
         181 tecaqtggcaqtgggtetgggacagacttcactetcaccatcagcagactggaqeetgaa 240
                                                                    178 ircasigedasigediciosancana acticación carcana 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligo-nucleotide(s) for inducing mutagenesis in an Ig light chain gene CDR - useful for prodn. of Ig heavy and light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 8.38e-137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 228; DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   T15203 standard; cDNA: 646 BP.
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Best Local Similarity 88.6%;
Matches 279, Conservative
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02-SEP-1994, US-300386.
(SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                         301 aaggtggaactcaaa 315
                                                                                                                                                                                                                                                                                                                                   298 AAGGTGGAGATCAAA 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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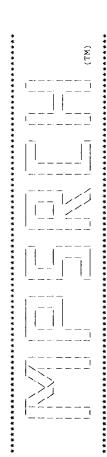
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111111111111111 | 11 | 111| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143^\circ gocagicagaptytiagoaacaacatagootggianoagoagaaaccigoonagarino: 202^\circ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         071872 encodes the light chain of a human type anti-19E peptide 071872 encodes the light chain of a human type anti-19E peptide monoclonal antibody which inhibits the signal transmission for the release of chemical mediator from mast cells and basophils stimulated with allergen. The antibody can be used for the prophylaxis and the therapy of allergy. 216 G; 195 T; Sequence 324 Br. 277 C. 216 G; 195 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human monoclonal anti-IqE peptide antibody - inhibits histamine release from mast cells by allergen stimulation, useful for
                                                                                                                                                                                                                                                                                                                                                              Human 1gE; CH4 region; triggers mediator release:
Mast cells; Monoclonal antibody; allergy; Immunoqlobulin; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scare 226; DB 10; 1 pred. No. 2.08e-135;
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                                                                                                                                                                                                                                                                                                   27-Ocr-1994 (first entry)
Sequence coding human anti-1gE MAD light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kobayashi F, Mizuno A, Morinaga T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product* antibody light chain
/note= "Human monoclonal anti-19E antibody "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note "C or G, illegible sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Q71872 standard; cDNA; 924 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 89.0%;
Matches 275; Conservative
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                                                      298 AAGGIGGAGAICAAA 312
301 aaggtggaactcaaa 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
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nt (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc. Release 2 1D John F Collins, Riocomputing Research Unit Copyright

Tue Feb 24 13:19:13 1998; MasPar time 215.47 Seconds 866.301 Million cell updates/sec n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Run on:

(1-378) from US08844215.seq 378 >US-08-844-215-27 not generated. Tabular output Description:
Perfect Score:
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1 GAGGIGCAGCIGCTCGAGIC

GESTORATOROGISTOTICA 378 SAGASCAGTOSCACAGAGAGAGA

TABLE default Gap 6

Scoring table:

665703 seqs, 246912890 bases x 2 Searched:

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Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

1. EST1 2. EST2 3. EST3 4. EST4 5. EST5 6. EST6 7. EST7 8. EST9 9. EST9 11. EST11 11.2. EST12 113. EST13 14. EST3 4. EST4 18. EST3 15. EST13 11. EST13 14. EST3 15. E

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180 ESTIRO 181 ESTIRI 182 ESTIRZ 183 ESTIR3
185:ESTIRS 186:ESTIRS 187:ESTIR7 188:ESTIR8
190 ESTI90 191 ESTI91 192:ESTI92 193:ESTI93
195:ESTI95 196:ESTI96
179.EST179 1
184:EST184 1
189:EST189 1
194:EST194 1
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Srale 5 289 Variance 1 980; Mean 9.944; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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                                   Ludarious, metazod; Enumerazod; Bitactia; Compata, Steichthyes, Sarcopterygi; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Butheria; Archonta; Primates; Catarrhin; Hominidae; Homo.

1 (hases 1 to 209)

2 Adams,M.D. Kerlavage,A P., Fleischmann, P.D., Fuldner; P.A., Malte,O., Sutton.G., Rlake,J.A., Wahnstock,K.G., Googane,J.D., White,O., Sutton.G., Rlake,J.A., Brandon, P.C., Chiu,M.-W.

Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J. Fine,L.D., Firzderadd,L.M., FitzHugh,W.M., Fritchman,J.L., Geodgagen,N.S.M., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle Jr.P.S., Kelley,J.M., Klimek,K.M., Kelley,J.G., Liu,L.T., Marmaros,S.M., Merrick,J.M., Noreno-Palanques,P.F., McDonald,L.A. Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Ordendary, T. Weddmari,J.F., Ui,Y. Pedrafk,D.P., Feng,P.P., Ferrie,A., Fischer,C., Hastings,G.A., Ryder,S.E., Scott,J.L., Utterback,T.F., Kim,A., Kozak,D.L., Greeda,M.A., Collins,E.-J., Dimke,D., Feng,P.P. Ferrie,A., Melssner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J. Grital Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of CDNA Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database
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The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
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Homo sapiens

ORGANISM

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Adams, M. D., Kerlavage, A. P., Floischmann, P. D., Fuldhorr, R. A., Adams, M. D., Kerlavage, A. P., Funderser, K. Gorcayno, I. D., White, O., Sutton, G., Blake, J. A., Frandon, R. C., Frie, L. D., Clayton, P. A., Chin, F. H., Friehman, T. J., Googhagen, N. S.M., FitzGerald, L. M., FitzHogh, W. M., Fritchman, T. J., Googhagen, N. S.M., Glodek, A., Goehm, C. L., Hanna, M. C., Heddlow, E. J., Fine, L. D., Kelley, J. M., Klimek, K. M., Kelley, J. C., Liu, L. J., Marmaros, S. M., Perleginos, P. F., McPonald, L. A., Marmaros, S. M., Perleginos, P. M., Pringer, D. T., Saudek, D. M., Shirley, R., Small, K. V., Spriggs, T. A., Utterback, T. K., Weidman, J. F., Li, Y. & Gooll, K. W., M. Gooll, K. J., Forrico, A., Fischer, C., Hastings, G. A., He, W. W., Hu, J. G., Greene, J. M., Grüber, J., Hudson, P. J., Thinke, P. Forrico, A., Grüber, C., Hastings, G. A., He, W. W., Hu, J. G., Greene, J. M., Grüber, J., Hudson, P. J., Raymond, L., Weis, Y. F. Wing, J. Xu, C., Yu, G. L., Puben, S. M., Dillon, P. J., Fannon, M. F. Fosen, C. A., Haseltine, W. A., Fields, C., Fraser, C. M., and Venter, J. C. M. Initial Assessment of Human Gene Diversity and Expression Patterns has a for the control of Connaccondenses of Thomas, M. M., Shannon, M. Schundon, M. A., Shannon, M. Sagnanon, C. M., M., Shannon, M. Springer, S. M., Dillon, P. J., Fornio, C. M., Anderson, C. M., Anderson, C. M., Anderson, C. M., M., Shannon, M. Springer, S. M., Dillon, P. J., Fornio, C. M., Anderson, C. M., M., M., Shannon, M. Springer, S. M., Dillon, P. J., Fornio, C. M., Anderson, C. A., M., M., M., Shannon, M. Springer, C. M., M., Shannon, M. Springer, C. M., M., M., M., Shannon, M. Springer, S. M., M., M., M., Shannon, M. Springer, C. M., M., Shannon, M.
Eukaryotae; Metazca, Eumetazca, Rilateria; Coelomata;
Deuterostomia, Chordara; Verrebrata, Gnathostomata; Ostelchthyws;
Sarcopterygii, Chomata, Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta, Primates; Catarrhini, Hominidae; Homo.
1 (bases 1 to 287)
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For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
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DEFINITION ESTR96669 Homo sapiens cDNA 5' end similar to immuneal-dealin heavy
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          932 Clopper Pd. Galthersburg, MD 20878
Tel: 3018699056
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         Deuterboundary, Prinates, Catarrhin; Hominidae, Homo.

Eutheria, Archonta; Primates; Catarrhin; Hominidae; Homo.

I (bases 1 to 238)

Bult, C.J., Lee, N. Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., Mitc. O., Sutton, S. Blake, J.A., Brandon, E.C., Chii, M. W., Cotton, M. D., Farla-Huphas, J. Fine, I. D. FitzGerald, L. M., FitzHugh, W. M., Fritchman, I. Geoghagen, N. S. M. Glock, A., Gnehm. C.L., Hanna, M.C., Hedblom, E. Hinkle Jr. P. S. Kelley, J.M., Moreno-Palaques, R.F., Mechanald, L.A., Ngiyen, N. S. M., Merrick, J.M., Moreno-Palaques, R.F., Mechanald, L.A., Ngiyen, D. T., Pellegrino, S. M., Phillips, C.A., Fyder, S. E., Scott, J. I., Weighan, J. E., Li, Y. Redarik D. P. Cao, L., Cepeda, M.A., Collins, E. J., Dimke, D., Feng, P., Ferrie, A., Gruber, J., Hudson, P. Kim, A., Kozak, D. L., Cheeda, M.A., Collins, E. J., Dimke, D., Feng, P., Ferrie, A., Gruber, J., Hudson, P. Kim, A., Kozak, D. L., Wing, J. Yu, C., Yu, C., L., Ruben, S.M., Dillon, P. J., Fannon, M.R., Rosen, C. A., Kasel, C. L., Ruben, S.M., Dillon, P. J., Fannon, M.R., Rosen, C. A., Tass, S. Olsen, H., Raymond, L., Wanna Gene Diversity and Expression Patterns Based Upon S. Million Basepairs of CDNA Sequence
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Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
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<1..>238
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Fred. No.
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DEFINITION me87g10 r1 Scares mouse 3NDMS Mus musculus cDNA clone 618594 5'
DEFINITION me87g10 r1 Scares mouse 3NDMS Mus musculus cDNA clone 618594 5'
Similar to qb:X14584 IG HEAVY CHAIN PPECURSOR V-III PEGION (HUMAN);
qb:V00821 Mouse mRNA fragment for immunoglobulin mu encoding the
of normalization to a Cot = 20. Library constructed by Bento Soares
                                                                                                                                 Deuterostonia: Chordata: Vertebrata: Gnathostomata: Osteichthyes; Sarcopterggii: Choanata: Tetrapoda: Amniota: Mammalia: Theria; Butheria: Archorta: Primales: Catarrini: Hominidae: Homo. (Dases 1 to 385)
Hiller, L., Clark, N., Dubnque, T., Elliston, K., Hawbins, M., Hulman, M., Kucaba, T., Elliston, K., Hawbins, M., Parsons, J., Psiffin, L., Pehiffin, L., Pehiffin, L., Pehiffin, E., Waterston, R., Williamson, A., Wohldmann, P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 aggtgcaggtngtgcagtctggggctgaggtgaagatgcctgggggcctcagtgaagcttt 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 ctgggacaagggattnagtggctgggactaatcaaccccggagtgatccca-cactcacc 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 CIGG-ACAAGGICTIGAGIGGAIGGGAGGCAICAIGCIAIGIIGGGAACAGCAAACIAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 CCTISCAGISISTICTIBISASICIAGABSTICABAAGIIASAAIIITGAAIIIGGGIGGGAGAGGGGG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 AGGIGCAGCIGCICGAGICIGGGICIGAGGIGAAAGCCIGGGICIICGGIGAAGGICI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 cetgeaaggeatetggattegegeteageeaceactacatgeactgggtgegaegggee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                          Eukaryotae; Metazoa, Eumetazoa; Bilateria; Coelomata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 5.34e-110;
0, Mismatches 74, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stops: 323 Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="187240"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WashU-Merck EST Project
                                      and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 21.2%;
Best Local Similarity 69.9%;
Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
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3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTTT3 vector. RNA provided by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M Fatima Ronaldo."
1 (bases 1 to 823)
Marra,M., Hillier,L., Allen,M., Howles,M., Dietrich,N., Dubuque,T.,
Masta,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="C57BL/6J"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gacgtgaagetggtggagtetgggggaaggettagtgaageetggaaggteeetgaaaete 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 tootgtgcagcotctggattcactttcagtagctatgccatgtcttgggttcgccagact 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CCTGGACAAGGTCTTGAGTGGATGGGAAGGAATCATCCTTA TGTTCGGAAGAAGAAGTA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 tgcagacactgtgaagggccgattcaccatctccagagacaatgccaggaacaccctgta 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 COCACAGAGITICAGGGCAGAGICACAAITACGGGGACGAAIGCAGGGCGACAGGGTA 239
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                                                                                                                                                                                                                                                                                                 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 67; DB 196; Length 823;
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| Mismatches 104,
                                                                                                                                                                                                                                                       WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares mouse 3NbMS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vector to vector length is 867
Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 492
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                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                 Email - mouseest@watson wustl edu
                                                                                                                                                    The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Spleen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="4 weeks"
/lab_host="DH10B"
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Best Local Similarity 63.3%;
Matches 183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208
                                                                                                                                                                                  Unpublished (1996)
                                                                                                                               Waterston, R.
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RESULT

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Vertebrata; Butheria; Artiodactýla; Suiformes; Suina; Suidae; Sus.
1. (bases 1 to 330)
                                                                                                                                                                                                                         Winteroe, A.K., Fredholm, M. and Davies, W. Evaluation and characterization of a porcine small intestine cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      so similar to the Megaph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="small intestine"
/clone_lib="directionally cloned cDNA in XL1-blue MRF'"
/clone="cld10"
                                                                                                                                                                                                                                                                                                                                                             Submitted (26-JUL-1995) Winterow A K., The Royal Veterinary and Agricultural University, Department of Animal Science and Animal Health, Division of Animal Genetics, Bulcwsvej 13, 1870 Frederiksberg C, DENMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 gaggagaaggtggtggagtctqgaggaggcctggtgcagnctgggnggtctctctdaqactc 117
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                                                                                 diversity region; EST; expressed sequence tag; immunoalobulin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GCACAGAAGITTCAGGGGCAGAGTCACAATTACCGGGAAGAGAGAAATCCGACGGGCACAGAGTAC 240
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                                                                                                        immunoglobulin heavy chain; joining region; variable region.
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                         clone cldlu).
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0: Mismarches 106;
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IG HEAVY CHAIN V-III REGION (HUMAN);.
                      S serofa mRNA: expressed sequence tad (5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                 Genome 7, 509-517 (1996)
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Matches 167; Conservative
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I and cloned into the Pac I and Ecc PI sites of the modified pi713
                                                                                                      Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Butheria; Archorda. Primates: Catarrhini, Hominidae. Homo.
Hillier.L., Clark.N., Dubuque, T., Elliston, K., Hawkins, M., Hultman, M., Kucaba, T., Elm., Lennon, G., Marra, M., Parsons, J., Fiftin, L., Pohffing, T., Sarres, M., Tan, F., Trevaskis, E., Waterston, P., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         yjjihog ri Homo sapiens chwa clone 156161 5° similar to gb.W62726
16 HEAVY CHAIN V-III REGION (HUMAN);
                         Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 TCAATTGGGTGCGACASGCCCCTGAAAAGTGTTGAATGAATGGGAAGGAAGCATCATCA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 atggaagtaataaatactactgcagactccgtgaagggccgattcaccatctccagagaca 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 IGTICGGAACAGAGAAAJIAGGGACAGAAGIIICAGGGIAGAGICACAAIIACGGGGGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 attecaagaacaegetgtatetgeaaatgaacageetgagagetgaggacaeggetgtgt 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 CTGGGTCTTCGGTGAAGGICTCCTGCAGGGCCTCTGGAGGCAGCTICAGAAGCTACAATT 100
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                  Library went through one round of normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                        Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 419;
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                                            constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                              WashU-Merck EST Project
Washington University School of Medicine
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/clone="214441"
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Source: IMAGE Consortium, LLNL
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Pred No
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                                                                                                                                                                                                                                                                                                      The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson wustl edu
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Local Similarity 61.8%;
nes 154; Conservative
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a 100 c
                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
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double-stranded oppNA was ligated to Et FI adaptors (Pharmacia), digasted with Not I and cloned into the Not I and Foo RI sites of modified pr713 vector (Pharmacia). Library went through one round of normalization to a Cot - 230. Library constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                    Devicestonia, Cherdata, Veriebrata, Snathostomata, Steichthyes, Sarcopterggii, Choanata, Tetrapoda: Amniota, Mammalia, Theria; Eutheria: Archonta; Primales; Catarrhini; Hominidae; Homo (bases 1 to 430)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Kucaba, T., E.M., Lennon, G., Marra, M., Parsons, J., Rikfin, L., Parsons, J., Rikfin, L., Walliamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 CTGGAJAAGGTGTTGAGTGGATGGAAGGCATGATGGGT-ATGTTGGGAAGAGGAAGTAC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 tigggagatgaccageetgacaggigaaagacaeggetgtgtattnactgtgnga 377
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Washington University School of Medicine
4444 Forest Park Parkway, Rox 8501, St. Louis, MO 53108
                                                                                                                                                                Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
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Local Similarity 62.9%; Pred. No. 3.54e-57;
es 185; Conservativo
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/clone="155161"
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Source: IMAGE Consortium, LLNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tral: 314 285 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1995)
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                                                                                                                                         Homo sapiens
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Deuterostomia; Chordata; Vertebrata; Gnathostomata; Ostelchthyes;

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modified pT713 vector (Pharmacia). Library went through one round of normalization to a Cot - 20. Library constructed by Bento Soares
                                                                                                   Eukaryotae, Metazoa, Eumetazoa, Bilateria, Coelomata,
Peuterostomia, Chordata, Vortebrata, Gnathostomata, ostolohthyos,
Sarospierpii: Choanata, Tetrapoda, Ambiota, Mammalia, Theria,
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Deuterostomia, Chordata, Vertebrata, Gnathostomata, Osteichthyes,
Sarcopterygli, Choanata, Tetrapoda, Amniota, Mammalia, Theria,
Eutheria, Archonta, Primates, Catarrhini, Hominidae, Homo,
1 (bases 1 to 478)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Hillier, L., Clark, N., Ku, aba, T., Le, M., Lennon, G., Marra, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL.
This clone is available royally-free through LLNL: contact the IMAGE Consortium (anto-final anti-final 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 ASAASTITIGAGGGGAGAHPAPATIAPPRAGAADGAAGGGAGGGGGGGTAGATGG 244
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                                                                                                                                                                                                                         Eutheria: Archonta: Primates: Catarrhini: Hominidae: Homo.

[hases 1 to 97)
Hillior,L., Clark,N. Dubuque,T. Flliston K. Hawkins,M.,
Holman,M. Hyltman,M. Kuraba,T., Lo.M. Lennon G. Marra,M.
Parsons,J., Rifkin,L., Fohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,E., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box RGG, St. Louis, Mo 64108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45; DB 69; Length 97;
Pred. No. 1.89e-42;
0; Mismatches 31; Indels
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                      and M Fatima Ronaldo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                               Homo sapiens
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Sarcoprerydii; Cheanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhin; Hominidae; Home.

E. (Bases I to 297)

S. Adams, M. D. 297)

S. Adams, M. N. Kerlavage, A. P., Fleischmann, P. D., Fuldner, P. A., Bult, C. J., Lee, N., Kirkness, E. F., Weinstonk, K. G., Gavague, J. D., White, O., Sutton, G., Blake, J. A., Brandon, R.C., Chiu, M. W., Cline, P. T. Cotton, M. D., Earle-Hughes, J. Fine, I. D., FitzGerald, I. M., FitzHugh, W. M., Fritchman, T. L., Geoghagen, N. S. M., Staldek, A., Gnehm, C. L., Hanna, M. C., Hedblom, E., Hinkle, Jr. P. S., Kelley, J. W., Klimek, K. M., Kelley, J. C., Liu, L. I., Marmaros, S. M., Marrick, J. M., Moreno-Palanques, P. E., McChonald, L. A., Nquyen, D. T. Pellegrino, S. M., Phillips, C. A., Payder, S. F., Scritt, J. I., Weidman, J. E., Li, Y., Bednarik, D. P., Gool, I., Cepeda, M. A., Colleman, T. A., Collins, E. J., Dinke, D., Feng, P., Ferrie, A., Hattings, G. A., He, M. W. W. 19, J. S., Greene, J. M. Fischer, G., Hattings, G. A., He, M. W. W. 19, J. S., Greene, J. M. Fischer, G., Hattings, G. A., He, M. W. W. 19, J. S., Greene, J. M. Fischer, G., Hattings, G. A., He, M. W. W. 19, J. S., Greene, J. M. Fischer, G., Hattings, G. A., He, M. W. W. 19, J. S., Greene, J. M. Fischer, G., Hattings, G. A., He, M. W. W. 19, J. S., Greene, J. M. J. S., Greene, J. W. J. S., Greene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database
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IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN);
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The Institute for Genomic Research
93z Clopper Rd, Gaithersburg, MD 20
Tel: 3018699056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Other_ESTs: THC23410
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Eukaryotae, Metazoa: Bumetazoa: Bilateria; Coelomata:
Eukaryotae, Metazoa: Bumetazoa: Bilateria; Coelomata:
Deuterostomia; Choanata; Tetrapoda; Amniota; Mammalia; Theria,
Barcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria,
Eutheria; Archonta; Primates; Catarrhini; Hominidae, Homo

1 (bases 1 to 299)
S Adams, M.D., Lee, N. Wirknes, E.F.; Wainstonk, K.G., Gorayne, P.A.
Bult, C.J., Lee, N. Wirknes, E.F.; Wainstonk, K.G., Gorayne, T.D., White, O., Sutton, G., Blake, T.A., Brandon, P.C., Chiu, M.-W., Claychor, R.A., Cline, M. T., Cotton, M.D., Barle-Heqhes, J., Fine, L.D., FitzGerald, L.M., FitzHugh, M.M., FitzFrhyman, J. J. Geoghagen, N.S.M., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr., P.S., Kelley, J.M., Mirmek, K.M., Kelley, J.C., Liu, L.-T., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, P.F., Mchonald, L.A., Nguyen, D.T., Pellegrino, S.M., Shirley, R., Shall, K. V., Spriggs, T.A., Utterback, T.P.
                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stops: 279
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image llnl.gov) for further information.
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4444 Forest Park Parkway, Box 8501, St. Louis, Mc 53108
Tel: 314 286 1800
Fax: 314 286 1810
Parsons,J., Rifkin,L., Rohlfing,T., Spares,M., Tan,F.,
Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 478;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
                                                                                       The WashU-Merck EST Project
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129 c 13
                                                                                                                                                                               Contact: Wilson RK
WashU-Merck EST Project
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Best Local Similarity 61.7%;
Matches 179; Conservative
                                                                                                                   Unpublished (1995)
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T64512 20-PEB-1995
gc24f06.rl Homo sapleds TDNA Glode 8167 57 similar to gl.M18512 13
HEAVY CHAIN PPECUPSOR V-I PEGION (HUMAN):.
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vector=PBluescript SK- host-SOLR cells (kamanycin resistant)
perimer=M13RPI Beitel=Ecopt Psite2=xhoI Normal lung tissue from a 72
year old male Cloned unidirectionally Primer: Olige dt. Average
linsert size; 1.0 kb; Uni: 2AP XR Vector: 5' adaptor sequence:
5'-GAATICGGCACGACA3; 3' adaptor sequence:
5'-CTCGAGTITITITITITITITITITI's'.
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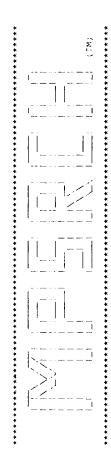
1 (bases 1 to 159)
Hillbert, Clark, N. Pubuque, T., Elliston, K., Hawkins, M., Holman, M., Hylman, M., Kurabo, T., Elliston, K., Hawkins, M., Parsens, J., Elfshin, L., Pohlfing, T., To, M., Trevaskis, E., Waterston, P., Williamson, A., Wohldmann, P., and Wilson, R., Washi-Merck, EST, Project
Weidman, J. F. Ji, Y., Rednarik, D. P., Gao, L., Cepeda, M. A., Collenan, T. A., Collins, E. T., Uimkel, L., Fengy, P., Perrie, J. M., Fischer, C., Haetings, G. A., He, W. -W., Hu, J. -S., Green, J. M., Grüber, I., Hudsen, P., Kim, A., Kozab, D. L., Kunsch, C., Ti, H., Li, H., Wassener, P. S., Olsen, H., Paymond, L., Wei, Y. F., Wing, J. Y., Xu, C., Yu, G.-L., Puber, S. M., Dillon, P. J., Famon, M. R., Possen, C. A., Haseltine, W. A., Fields, C., Fraser, C. M., and Venter, J. C., Initial Assessment of Human Gene Diversity and Expression Patterns Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: tdbinfo@tdb.tigr.org
for clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org).
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4444 Porost Park Parkway, Pox 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                             The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699656 Exx; 3018699423 Email: +4-1
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Rest Local Similarity 64.8%; Pred. No. 7.196-39
Matches 94; Conservative 0; Mismatches 5
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WashU-Merck EST Project
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ypl1g03 rl Homo sapiens onna clone 187156 5' similar to qb-M62725
IG HEAVY CHAIN V-III REGION (HUMAN);.
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                                      High qality sequence stops: 139 Source: IMAGE Consortium, LLNL
This clone is available ropalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; Metazoa; Eumetazoa, Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Grathostomata; Osteichthye Sarcopterygli; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Frimates, Catarrhin; Hominidae; Homo. 1 (bases 1 to 303) Frimates, Catarrhin; Hominidae; Homo. Hillier, L., Clark, N., Dubuque, T., Eliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, P., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501. St. Louis. MO 63108
                                                                                                                                                                                                                                                                                     Length 169;
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Pred No. 7,40e-32;
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                                                                                                                                Location/Qualifiers
                  Email: est@watson.wustl.edu
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Best Local Similarity 81.4%;
Matches 57; Conservative
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Fax: 314 286 1810
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Fax: 314 286 1810
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and closed into the Not I and Eco RI sites of a modified pT713 vector (Pharmacia). Library went through one round of accmalication to a rot \sim 20^{\circ} library constructed by Fonto Soaros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yo70g05.rl Homo Sapiens CDNA clone 183320 5' similar to qb:s55735
IG ALPHA-1 CHAIN C REGION (HUMAN);.
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Sarcopterygii; Choanata; Tetrapoda; Amniota: Mammalia; Theria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human cloue-183320 library=Soares breast 3NbHBst vector-pTTTO (Pharmacia) with a modified polylinker host-0910R (ampicillin resistant) primer=MT3PFD PSi.ch=Wrt 1 PSi.ch=Eco RI Adult human. Ist strand CDMA was primed with a Not I - oliquo(dT) primer [5' TGTTACCAAPTSAAGTGGGAGGGGCTTTTTTTTTTTTTTTTTTTTT 3'],
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty free through LLNN. . contact the IMAGE Consortium (info@image.llul.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 ayatgoagotyyanyaytotyyyyyaaqoytgatroagootgaaaaytoootaaaactot 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 octytgdayddtetgyattdagdttdagtgaytatyqdagggdadtagggtarconnoganone 231
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Farsons,J., Rifkin,L., Nohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                              Length 403;
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Pred. No. 4.46e-25;
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                                                                                                                                                                                                                    Mismatches
75.0
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                                                                                                                              Score 39;
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Hillier, L., Clark, N.
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Best Local Similarity 63.8%;
    U
                                                                                                                                                                  Local Similarity 62.2%;
nes 89; Conservative
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Fax: 314 286 1810
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Release 2.1D John F. Collins, Biocomputing Pesearch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by intelligenetics, inc. MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Publich. The Peb 24 of 01 (1998, Mashar time 6.87 Seconds 266 970 Million cell updates/sec

Tabular output not generated.

Title: >US-08-844-215-1 Description: (1-132) from US08844215.pep Perfect Score: 956

Sequence: 1 EVQLLEQSGAEVRKPGSSVK.....RCYPGFFQQWGQGTLVTVSS 132

PAM 150 Gap 11

Scoring table:

Searched: 111726 segs, 13989129 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq30

l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 17:part17 18:part18 19:part19 20:part10 21:part11 12:part18

Statistics: Mean 30.954; Variance 153.640; scale 0.202

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Query					
Score		Match	Match Length	DB	ID	Description	Pred. No.
9		72.8	481	Ŋ	R24442	Sequence of antibody	1.37e-47
		58.5	120	ch	R54796	SpA-reactive IqM heav	4.30e-36
557		58.3	476	9	R31023	(A)	6.32e-36
4		57.4		ca Ca	W19888	CEA-specific antibod;	2.94e-35
537		56.2	96	15	R72058	DP10 VH region.	2.94e-34
534		55.9	123	23	MIGRAI	Jöds	
533	m	5	CI	23	W19889	CEA-specific antibody	6.34e-34
533	٠.	55	K. C.T.	۲,	MIORPT		
53	<i>~</i> .	5.5.4	123	64	W. SBBB	CEA-specific antibody	1.130-33
52	σ	55.3	147	12	R65019	93KA9 anti-Varicella	1.376-33
52.5	vc.	ر. الا	c.	ď	W13526	Anti-melanoma antibod	2.430-33
RJ C4	~ 4	54.5	-H	œ,	F45610	Monoclonal antibody G	~
E i			9.8	C 4	6500244	HV126? VH region.	2.00e-32
51	'n	m	117	4	R22358	Protein encoded by th	2.00e-32
51	Ŋ		-	7	R38623	Human heary chain V r	.00e-3
5	L)	53.9	$\overline{}$	50	W03950	DNA fragment vh49 8,	2 00e-32
51	10	ω,	122	-1	F75964	HSV-neutralising anti	2.00e-32
51	m	53.7	120		P54795	SpA-reactive IqM heav	26-956 3
CI L'		2.5		::	P11874	Himanised mouse DPC-2	3 546-35
ed u)	٠,	53.6	140	σ,	P. 5.5.5.6	DPEG-200 Humanized an	3,546-32

	6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6. 6
Human anti-tumour ant Human ised heavy chain Human ised 5G1 1 VH + Human ised 5G1 1 VH + Human antibody Eu hea Human sed 5G1 1 VH + Human sed CDP-grafted Humanised CDP-grafted Humanised 5G1 1 VH + Humanised AG2 1 PH + Humanised AG3 1 PH + Humanised CG3 1 PH + Humanised Ph + COMPLETELY HUMANISED HOA Humanised Humanised Hea Humanised W Human rh Pre-5AB humanised hea Humanised W Humanised Hea Humanised Humanised Heavy CY1748PHR VH FFG100 PH +	RI.3/Humanised he Y1748RHA VH regio umanised X291 ant
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ALIGNMENTS

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Disclosure, Fig 1, 46pp, English.
The 1301, in its nascent form, bears no sladyl-tex side chains. The inverture designed a mclee-licituding several such situe for altachment of sladyl-tex side chains (see R24442, FT). The
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18 NOV-1991.

18 NOV-1991.

18 NOV-1991.

18 NOV-1991.

20-NOV-1991.

Scal B. Walz G.

WALZ 92-215789/26.

WALZ 92-20548.

Inhibition of cell adhesion mediated through ELAM:1 mol. binding used in treating chronic inflammation, rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                       /label= N
/note= "Substn. to create glycan addition site"
Misc_difference 310
                                                                                                                                                                                                                                                               Key Location/Qualifiers Misc_difference 308
                                                                                                                   02-JAN-1992 (first entry)
Sequence of antibody molecule 1gGl.
Antibody; immunoglobulin Gl.
Homo sapiens.
LT 1
R24442 standard; Protein; 481 AA.
R24442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc_difference 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= S
/note= "see above"
Misc_difference 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "see above"
Misc_difference 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc_difference 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc_difference 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= S
/note= "see above"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /notem "see above"
W09209293-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label * N
/note * "see above"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label = N
/note= "see above"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           psoriasis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label- N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 AQNYAQKERDRVSIIADESTSTIELSNLRSDDTAVYYCARDPPRYCSAGRCYPGFFQQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 94-167127/20.

WPI; 94-167127/20.

Stimulating prodn. of variable region gene family restricted antibodies - through B-cell super-antigen vaccination Disclosure; Fage 78; 130pp; English.

A B-cell superantigen (849) is a fragment of SpA D domain that specifically binds the Fab portion of variable region restricted antibodies. The SAG is used to enhance production of VH; especially antibodies. Thuring attempts to identify sAGs, as sequences (R54784-801) of H chains from Ig reactive with mod SpA, and as and DAS sequences (R4801).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 vhlv-qsgaevkkpgssvkvsckasggtfssyaiswvrqapggglewmggiipifg--g- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 yaq----kfggrvtitadeststaymelsslrsedtavyycardngaycsggscysgwfd 139
                                                                                                                                                                                                                                                                                                                                                                 61 YAQNYAQKFRDRVSIIADESTSTSFIELSNLRSDDTAVXYCARDPPRYCSAGRCYPGFFG 120
additional N-linked qlycosylation sites are introduced at locations which impair complement fixing and Fc receptor binding ability. They are preferably located in the CH2 region of the Iq molecule. Antibodies bearing multiple slalyl-Lex determinants are useful for disrupting undesirable interactions between cells or proteins. Disrupting this interaction has therapeutic applications, for example, in minimising inflammation following tissue injury.
                                                                                                                                                                                                                                                                                                       1 EVOLLEQSGAEVRRPGSSVKVSCKASGGTFSGHVITWVRQAPGQGLEWMGESIPIFGSAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Indels 11; Gaps
                                                                                                                                                                                                                                                                  qvqlv-qsgaevkkpgssvkvsckasggtfssyaiswvrqapggglewmggiipifgtan 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SpA-reactive Ign heavy chain clone KAS.
SpA demactive Ign heavy chain region; Ign. B-cell superantigen; SAG;
superantigen; heavy chain variable region; VH3 restricted antibody;
VH; protein-A; KAS; B-lymphocyte; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IgM protein
                                                                                                                                                                                                                              5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    obtained from combinatorial libraries were determined. IgM
KAS is derived from the germline configuration of a VH gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 58.5%; Score 559; DB 9; Length 120; Local Similarity 68.7%; Pred. No. 4.30e-36; hes 90; Conservative 16; Mismatches 14; Indels 1
                                                                                                                                                                                  Score 696; DB 5; Length 481; Pred. No. 1.37e-47;
                                                                                                                                                                                                                           16; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T
P54796 standard: peptide: 120 AA
                                                                                                                                                                                         72.8%;
Local Similarity 75.0%;
hes 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGC ) UNIV CALIFORNIA.
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122 WGOGTLVIVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 wgqgtlvtvss 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 OWGQGTLVTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                      140 pwgqgtlvtvss 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-MAY-1994.
29-OCT-1993; U10555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Silverman GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09409818-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-0CT-1994
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                                                                                                                                                                                                  Query Match
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Disclosure; Fig 2: 35pp; English.

Disclosure; Fig 2: 35pp; English.

The sequences given in Kil023-24 represent the heavy and light, chaims of Antibody D is a monoclonal antibody which of Antibody D is a monoclonal antibody Which was derived from peripheral blood 'imphocytes from a hepatitis A virus (RAV) sero positive patient. Antibody D is closely related in nature to murine antibody BSB3. Total RNA was isolated from antibody D expressing cells and polyademylated RNA was extracted. These polyA RNA's were used to prepare a cDNA library which was screened for human kappa light (L) chains and two positive clones were detected. Sequence 476 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVĄELLEGSGAEVKKPGSSVKVSCKASGGTFSCHVITWVPQAPGGGLEWMGESIFIFGSAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 gmgvv-gsgaevkkpgssvtvsckasggtfsnyaiswvrqapgglewmggiipligtpt 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Gaps
                                              Heavy: light; chain; antibody; D; monoclonal; peripheral; blood;
lymphocyte; hepatitis A virus; HAV; sero; positive; patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prodn. of recombinant primate antibodies - useful for treating
infections caused by hepatitis A, B and C, herpes,
cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,
                                                            lymphocyte; hepatitis A virus; HAV; sero; positive; pulient; murine; B5B3; polyadenylated; CDNA library; human; Kappa; L; H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 557; DB 6; Length 476;
Pred. No. 6.32e-36;
19; Mismatches 23; Indels
                                                                                                         Location/Qualifiers
R31023 standard; Protein; 476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.3%;
Local Similarity 64.4%;
Les 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (WELL ) WELLCOME FOUND LID.
                           19-MAY-1993 (first entry)
                                                                                                                                                                                                                                                                                                             122..132
                                                                                                                                                                                                                                                                                                                                         133..241
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                                                                                                                                                                                                                                                                                                                                                                                                                     380..497
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15-JUL-1991; GB-015284.
01-AUG-1991; GB-016594.
                                                                                                                                   "Signal peptide"
                                                                                                                                                                                                                                                         85..113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-1992; GB-006284
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                                           Antibody D heavy chain.
                                                                                                                                                  20..49
                                                                                                                                                                                                                               69..84
                                                                                                                                                                                                     55..68
                                                                                                                                                                            50..54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crowe JS, Lewis AP;
WPI; 93-019951/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; 035099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arthritis etc.
                                                                                                                                                                                                                                                                                                                                                                                /label= HINGE
                                                                                                                                                                                                                                                                                                 CDR3
                                                                                                                                                                                          /label= CDR1
                                                                                                                                                                                                                                             /label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                          /label- CH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP-523949-A
                                                                                                                                                                                                                                                                       /label- FR3
                                                                                                                                                                                                                                                                                                                             FR4
                                                                                                                                                                                                                                                                                                                                                      'label= CH1
                                                                                                                                                                                                                                                                                                                                                                                                                                     CH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JAN-1993
                                                                                                                                                               label= FR1
                                                                                                                                                                                                                     /label- FR2
                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                            /label=
                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                    /label=
                                                                                                                                         'note=
                    R31023;
                                                                                                                                                                                                                                     Region
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                                                                                                                                                                                                                                                                                                                                                                                                Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This polypeptide sequence comprises the heavy chain variable region (VH), HBBIL, obtained by mutagenesis of the VH CDFT of human carcinombryonic antigen (hCBA) -specific antibody CEAG (see W19881). A Claimed specific binding member (A) comprises an hCEA specific antibody antigen binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 - 8 W, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 extracellular domain of hCEA and/or to cell-associated hCEA over the hCEA over soluble hCEA. Preferred (A) include pairings of VH and CV L sequences from CEA1-7 (see W19876-85), or their CDR sequences, as well as CEA6 VH and VL variants (see W19886-95) obtained by mutagenesis or chain shuffling. An example of a claimed pairing is HBBIL VH with CEA6 VL. (A) is used to detect cells expressing hCEA, in vivo or in vitto, especially tumour cells for diagnosing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YAQNYAQKFPDRVSITADESTSTSFIELSNLPSDDTAVYYCAPRPPPRYCSAGPCYPGFFQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 yaq----kfqgrltitadeststaymelsslrsedtavyycarhnhny-el-yyy--ymd 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 qvqlv-qsgaevkkpgssvkvsckasgqtfsnspinwlrqapgqqlewmgsilpsfgtan 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVOLLEQSGAEVPKPGSSVKVSCKASGGTFSGHVITWVRQAPGGGLEWMGESIPIFGSAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Specific binding members for human carcinoembryonic antigon · bind to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells, used for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 549; DB 23; Length 123;
Pred No 2,946-35;
16; Mismatches 19; Indels 9
                                                                                                  07-0FC-1997 (first entry)
CEA-specific antibody CEA6 VH mutant HBB11 sequence.
Carcinoembryonic antigen; CEA; human; antibody; scFv;
tumour marker; lung cancer; breast cancer; colon cancer;
                                                                                                                                                                                                                                                       /note- "complementarity determining region 1"
Region
                                                                                                                                                                                                                                                                                                   "complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                /note= "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Osbourn JK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                                                                                                                             Location/Qualifiers
                                                           л 4
W19888 standard; Protein; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Fig 2; 128pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 66.7%.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McCafferty JG,
                                                                                                                                                                  adenocarcinoma; diagnosis.
                                                                                                                                                                                 Chimeric Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                        11-02T-1996) GB-021295.
07-DEG-1995; GB-025904.
23-MAY-1996; GB-010824.
            121 SWGGGTLVTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 vwgggtmytvss 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ewagarryrss 132
                                                                                                                                                                                                                                                                                                                                                                                             09-DEC-1996; G03043.
                                                                                                                                                                                             Chimeric synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 97-319779/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 AA;
W09720932-A1.
                                                                                                                                                                                                                                                                                     /label- CDR2
                                                                                                                                                                                                                                                                                                                     Region
/label= CDR3
                                                                                                                                                                                                                                       /label- CDR1
                                                                                                                                                                                                                                                                                                                                                                             12-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Allen DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sednence
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                                                                                         W19888;
                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                             Region
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RESULT

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1 qvqlv-qsgaevkkpgssvkvsckasqqtfssyaiswvrqapqqqlewmggiipifqtan 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 537, EB 12, Length 98;
Pred. No. 2.94e-34;
13; Mismatches 6; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                       Graves' cphthalmopathy-associated monoclonal antibody - produced by molecular cloning of immunoglobulin genes by PCR by molecular cloning of immunoglobulin genes by PCR becourer, Page 68: 94pp; English.

L- and H-chain DNA was amplified by PCR from Graves' orbital tissue and clones encoding autoimmune-associated immunoglobulin fragments were obtained. 13/15 clones of H chain (1961) genes showed homology to the closest germline genes, DF12 (2022) and PH1253 (202320). The DNA (2009322) and corresp. amino acid OF7H1.2, are provided.

Sequences of the VH region of a representative clone, Sequence 98 AA:
                                                                    Graves ophthalmopathy associated immunoglobulin protein; orbital antigen; monoclonal antibody; heavy chain; H chain; variable region; autoimmunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W19881;
07-DEC-1997 (first entry)
CEA-specific antibody CEA6 VH sequence.
Carcinocmbryonic antigen, CEA; human; antibody; scFv;
tumour marker, lung cancer, breast cancer; colon cancer;
adenocarcinoma; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "complementarity determining region 1"
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Region 99.112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 31...35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                 30-MAR-1995.
22-SEP-1994; U10756.
22-SEP-1993; US-124469.
(NICH-) NICHOLS INST DIAGNOSTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W19881 standard; Protein; 123 AA.
R72068 standard; Protein; 98 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 76.7%;
Matches 79; Conservative
                                    (first entry)
                                                                                                                                                                                                                                                                                                                           Rapoport B;
                                                                                                                                                                                                50..66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31..35
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                                                                                                                                                                                                                                                                                                                       Mclachian SM, Rapo
WPI; 95-139383/18
                                  26-SEP-1995 (1
DP10 VH region
                                                                                                                                                                                                                                                                                                                                                             N-PSDB; Q89327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                           Homo sapiens
                                                                                                                                                                              /label= CDR1
                                                                                                                                                                                                                   /label- CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= CDR1
                                                                                                                                                                                                                                WO9508336-A.
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Allen DJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVQLLEQSGAEVRKPGSSVKVSCKASGGTFSGHVITWVRQAPGQGLEWMGESIPIFGSAN 60
                                                                                                                                                       This polypeptide sequence comprises the heavy chain variable region (VH) of human carcinoembryonic antigen (hCEA)-specific antibody CEA. VH (T72126-32) and VL (T7213-35) gene sequences were obtained for anti-hCEA antibodies CEA1-CEA7 (see W19876-85). A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 -8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 extracellular soluble hCEA. Preferred (A) include pairings of VH and VL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 gvqlv-gsgaevkkpgssvkvsckasggtfsnspinwlrgapggglewmgsiipsfgtan 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                          Specific binding members for human carcinoembryonic antigen \cdot bind to the A3-B3 extracellular domain of hCEA and are substantially
                                                                                                                                                                                                                                                                                                                                                                                               sequences from CEA1-7, or their CDP sequences, as well as CEA6 WH and VL variants, including combinations of CEA6 VH with VL regions from CEA6, ToROB4, TOROB5, TOROB12, LORIC, LORI7 or LOSC2.

(A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for diagnossing cancer, e.g. adenocarcinoma
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                                                                                         non-cross-reactive with human liver cells; used for diagnosing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumour marker, lung cancer, breast cancer; colon cancer; adenocarcinoma; diagnosis.
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CEA-specific antibody CEAA_VH mytant HBBA sequence
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                                                                                                                                        Claim 4; Fig la; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the colon, lung or breast.
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07-DEC-1995; GB-025004.
23-MAY-1996; GB-010824.
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WPI; 97-319779/29.
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                      N-PSDB; T72131
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This polypeptide sequence comprises the heavy chain variable region (VH), HBB6, obtained by mutagenesis of the VH CDR3 of human carcinomehyponic antigen (hCBA) specific antibody CEA6 (see W19881). A claimed specific binding member (A) comprises an HCBA specific antibody antigen binding demain that has a dissociation of specific antibody antigen binding demain that has a dissociation of constant for hCBA of less than 1 x 10 -8 M. Is non-cross-reartive with human liver cells, and preferentially binds to the A3-B4 extracellular domain of hCEA and/or to cell-associated hCEA over hCEA cover soluble hCEA. Preferred (A) include pairings of VH and VL sequences from CEA1-7 (see W1986-95), or their CBS sequences. as well as CEA6 VH and VL variants (see W1986-95) obtained by mutagenesis or chain shuffling. An example of a claimed pairing the HCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenocarcinoma of the colon. Uning or breast.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVQLLEQSGAEVPKPGSSVKVSCKASGGTFSGHVITWVPQAPGGGFFWMGESIPIFGSAN 60
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This polypeptide sequence comprises the heavy chain variable region
(VH), HBA11, obtained by mutagenesis of the VH CDR3 of human
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non-cross-reactive with human liver cells; used for diagnosing
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tumour marker; lung cancer; breast cancer; colon cancer;
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Pred. No. 6.34e-34;
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W19887 standard; Protein; 123 AA.
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                                                                     laim 4; Fig 2; 128pp; English.
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Best Local Similarity 65.9%;
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23-MAY-1996; GB-010824.
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Chimeric synthetic
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60 yaq----kfqgrltitadeststaymelsslrsedtavyyca-gans-cn--rsyyyymd 111
                                                                                                                                                                                                                                                                                        Score 532; DB 23; Length 123;
Pred. No. 7 68e-34;
19; Mismatches 17; Indels 9; Gaps
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carcinoembryonic antiqen (hZEA)-specific antibody CEA6 (see W19881). "A claimed specific binding-member (A) comprises an hCEA specific antibody antiqen binding-domain that has a dissociation constant for hCEA of less than 1 x 10 - 8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 extracellular domain of hCEA and/or to cell-associated hCEA over scluble hCEA. Preferred (A) include pairings of VH and VL sequences from CEA1-7 (see W19876-85), or their CDR sequences, as well as CEA6 VH and VL variants (see W1986-55) obtained by mutagenesis or chain shuffling. (A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenorarinoma of the colon, lung or breast.
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This polypeptide sequence comprises the heavy chain variable region (VH), ToEDIO, obtained by mutagenesis of the VH CDR3 of human carcinoembryonic antigon (hCEA)-specific antibody CEA6 (see W1981). A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 - 8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 extracellular domain of hCEA and/or to cell-associated hCEA over
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carrincembryonic antigen: CEA; human; antibody; soFv;
tumour marker; lung cancer; breast cancer; colon cancer;
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CEA-specific antibody CEA6 VH mutant T06D10 sequence.
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//section
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY Allen DJ, McCafferty JG, Osbourn JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T 9
W19996 standard, Protein, 123 AA.
                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 65.9%;
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adenocarcinoma; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-00T-1996; OR-021295.
07-DEG-1995; GR-025004.
23-MAY-1996; GR-010824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric Homo sapiens;
Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 vrgqgtmrtvss 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-DEC-1996; G03043
                                                                                                                                                                                                                                                      123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02/02/012-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "comp]
wog720932-Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label* CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7991-NUL-2
                                                                                                                                                                                                                                                        Sequence
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61 YAQNYAQKFEDRVSIIADESTSTSFIELSNLRSUDIAVYYCARDFFKYGSAGRCYPGFFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               claim 8: Fig 4B; 39pp; English.
A human anti-Varicella zoster virus monoclonal antibody was prepd.
using the tricma method of Ostborg of al. (1983) Hybridoma 2.361-367.
One resultant trioma neutralised VZV in the absence of complement.
This cell line, designated cell line 1C98RAP, produced an antibody designated 93RAP on the light and heavy chain variable region heavy chain (gamma-1) and two light chain (kappa) specific clones sequenced (see 082749 s Q82750 respectively).
                                                                                                                                                                                                                                                   1 qvqlv-qsgaevkkpgssvkvsckasggtfsnspinwlrqapggglewmgsiipsfgtan 59
                                                                                                                                                                                                                                                                                       1 EVQLILEQSGAEVPKPGSSVKVSGKASHGTFSGHVITWVPGAPGGGLEWMGFSTPIFGSAN 60
httpA over soluble httpA. Freferred (A) include pairings of VH and VL sequences from CBA1-7 (see W19876-85), or their CDR sequences, as well as CBA5 VH and VL variants (see W1986-95) obtained by mutagenesis or chain shuffling. Lamples of claimed pairings are 105D10 VH with 105D12 or CBA6 VL. (A) is used to detect cells expressing httA, in vivo or in vitro, especially tumour cells for diagnosting cancer, e.g. adenocarcinema of the colon, lung or breast.
                                                                                                                                                                                                             9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Varicella zoster virus; VZW. anti-VZW meneclenal antibody, 99KA9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93KA9 anti-Varicella zoster virus antibody heavy chain variable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human monoclonal antibodies specific for the glyco:protein II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subjunit of varicella coster virus - used in a therapy and prophylaxis of infection
                                                                                                                                                                      Score 530; DB 23; Length 123: Pred. No. 1.13e-33;
                                                                                                                                                                                                             17; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= complementarity determining region (CDR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alycoprotein II subunit; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R65019 standard; Protein; 147 AA. R65019;
                                                                                                                                                                    Query Match 55.4%;
Best Local Similarity 65.9%;
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein 20..147
/label= mature light chain
Region 50..54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SANO ) SANDOZ PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUL-1993; US-098479.
24-MAR-1994; US-217918.
                                                                                                                                                                                                                                                                                                                                                                                                   112 vwgqgtmvtvss 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ostberg L:
                                                                                                                                      123 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pegion
/label= CDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
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20, Mismatches 20, Indels 8; Gaps

**Match 55.3%; Score 529; DB 12; Length 147; Local Similarity 64.2%; Pred. No. 1.37e-33; les 86; Conservative 20; Mismatches 20; Indels 8

Query Match

Matches

g

20 gygly-gsgaevkkpgssykysckasggtfsnfaiswyrgapggglewmgrimplfyts- 77

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Claim 19; Page 75.76; 82pp; English.

A process for isolating and synthesising human monoclonal anti-tumour antibodies has been produced. The process involves: (a) constructing at least one fusion phage library from the peripheral blood lymphocytes the page library from the peripheral blood lymphocytes the page library from the peripheral blood lymphocytes the page library in a binding assay with cultured tumour antibodies in the phage library in a binding assay with cultured tumour antibodies in seep (b) and (c); (e) assaying the specificity of the cloned phage by incubating the phage with at least two types of cultured normal cells; and (f) further testing the specificity of cloned phage that do not bind to cultured tumour cells derived from more than one other tumour that is not the patient's tumour. The present sequence represents a human heavy continued tumour cells derived from more than one other tumour that is not the patient's tumour. The present sequence represents a human heavy and method as described above. The antibodies produced can be used for diagnostic and therapeutic applications and for isolating tumour more than one as an incommon for continued to the theory is a method as described above. The antibodies produced can be used for antipone from the patient's tumour general represents and for isolating tumour more than one as an anti-cancer vaccines.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               murine monoclonal antibodies (MAbs). Since the antibodies are isolated from fusion phage libraries, their affinity and specificity for a tumour cell line can be improved by genetic manipulations.
                                              78 -t--yaqkfqgrvtisadaststaymelsslrsddtamyycardita-pgaaptplnfyg 133
                                                                       1 EVOLLEQSGAEVPKPGSSVKVSCKASGGTESGHVITWVRQAPGGGLEWMGESIPIFGSAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 gglevkkpgssvkvsckasggtfssyalswvrqapggglewmggilpifgtanyaq---- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 SGAEVRKPGSSVKVSCKASGGTFSGHVITWVRQAPGQGLEWMGESIPIFGSANYAQNYAQ 67
                                                                                                                                                                                                                                                                                                                               28-0CT-1997 (first entry)
Anti-melanoma antibody 2-71 from VH antibody fusion phage library.
Human: monoclonal antitumour antibody; peripheral blood lymphocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prodn. of human monoclonal anti-tumour antibodies · by screening a fusion phage library produced using peripheral blood lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The human antibodies have low immunogenicity in humans compared to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.0%; Score 526; DR 23; Length 119, 69.6%; Pred No 2 43e-33; cative 16; Mismatches 10; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                              tumourigenesis; anticancer vaccine.
                                                                                                                                                                                                                                                                                         W13536 standard; protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID • R45610 standard; Protein; 124 AA. AC PA5610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87; Conservative
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30-JUN-1995; US-497647.
(UYYA.) UNIV YALE.
Cai X. Garen A:
                                                                                                                                            134 mdvwgqgttvtvss 147
                                                                                                                                                                                          120 QQ-WGQGTLVTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from a cancer patient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 VTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09702479-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                 cancer;
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60 ysqnf-q---grvtltadeststvymelsgltsadtavyycaksqaqwsnlirs-p--id 112
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Claim 6; Page 22-23: 34pp; English.

The monoclonal antibodies (MAb's) designated GP13, GP44 and GP68

react with HiV-1 gp120 glyoptotein variants containing the amino acids Asn88, Lys17, Asn262 and Tyr 435 but exhibit at loost for reduced reacton with gp120 variants in which these amino acids have been deleted or substituted. The MAb's are useful for passive immunotherapy and their anti-idiotypic antibodies can be used in the production of vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 gvglv-gsgaevkkpgssvkvsckasggtfssstlnwvrgtpggglewmgkiiptlusst 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLLEQSGAEVPKPGSSVKVSGKASAGTFSAHVITWVPQAPQQGFFWMAF51PTFGSAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Squa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monoclonal antibodies to HIV-1 - directed against diycosprotein
gp120, useful for passive immunotherapy or prodn. of
anti-idiotype vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a;
22-JUL-1944 (first entry)
Monocolonal antibody GP68 heavy chain (V H I).
MUL Human Immunodeficiency Virus; gp120; dlycoprotein;
envelope protein, manacional antibody MAN: vaccine; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  orbital antigen; monorlonal antibody; heavy chain; H chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 521; DB 9; Length 124;
Fred. No. 6.32e-33;
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                                                                                                                                                Location/Qualifiers
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31..35
                                                                                                                                                                                                                                                                                                                                                                                       /label- Framework IV. JH4 segment.
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(NICH-) NITHOLS INST DIAGNOSTICS.
McLachlan SM, Rapoport B;
WPI; 95-139383/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NEWE-) NEDERLANDEN. MIN WELZIJN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R72069 standard; Protein; 98 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.5%;
62.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 52.54.
83; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 QWGQGTLVTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-1993; 201959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-SEP-1994; U10756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Osterhaus ADME;
WPI; 94-036603/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HV1263 VH region.
                                                                                                                                                                                                                                                                   /label= CDR 2.
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                                                                                                                                                                                                                                                                                                                            CDR 3.
                                                                                                                                                                                                           'label - CDR 1
                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label- CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-FEB-1994
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30-MAR-1995.
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                                                                                                                                                                                                                                                                                                                               /label=
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Scarch completed: The Feb 24 07:03:57 1098 Job time : 41 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SENP-) GENPHARM INT INC.

LODDER N. KAY R.

Not. 22 113962/14.

P. N-FDSR: G22419

Immunoglobulin trans.genes - for prodn. of heterologous

In on-rearranged and/or rearranged ig chains.

Example 14; Page 87; 112pp; English.

C. The human placental genomic DNA library cloned into the phage vector lambda FIX II was screened with the human VHI family cortor lambda FIX II was screened with the human VHI family coperitic oligonucleotide (see Q22418). Phage clone lambda C399016 of the phage clone lambda common the sequence of the phage clone is a specific oligonucleotide of 6.1 kb Xbal fragment contg. the variable sequence the phage clone of this insert was sequenced. VH49:8 was found to have an open reading frame which encoded the sequence shown.
                                                                                                                                                                                                                                                                                                                                               1 qvqlv-qsgaevkkpgssvkvsckasggtfssyaiswvrqapggglewmgriipilg-i- 57
                                                                                                                                                                                                                                                                                                                                                                       20 gvglv-gsgaevkkpgssvkvsckasggtfssyaiswvrgapggglewmgriipilg-i- 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLLEQSGAEVRKPGSSVKVSCKASGGTFSGHVITWVRQAPGQGLEWMGFSIPIFGSAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                        5, Gaps
                                                                   L-and H-chain DNA was amplified by PCP from Graves' orbital tissue and clones encoding autoimmune-associated immunoglobulin fragments were obtained. 13/15 clones of H chain (IgG1) genes showed homology to the closest germline genes, DP10 (089328) and hv1262 (089328). The DNA (089329) and corresp. amino acid (R72070) sequences of the VH region of a representative clone, sequence 98 AA.
                 'ophthalmopathy-associated monoclonal antibody - produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-AUG-1992 (first entry)
Protein encoded by the human heavy chain V region gene VH49.8.
Heavy chain: variable region; VH1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 515; DB 4; Length 117; Pred. No. 2.00e-32;
                                                                                                                                                                                                                                                                 Length 98
                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-NOV-1993 (first entry)
Human heavy chain V region VH49.8.
Immunoglobulin; IgG; heavy chain; minilocus transgene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 YAQNYAQKEPDEVSIIADESTSTSFIELSNIPSDDTAVYYCAP 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 -a-nyaqkfqgrvtitadkststaymelsslrsedtavyycar 117
                                    by molecular cloning of immunoglobulin genes by PCR Disclosure; Page 69; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               58 -a-nyaqkfqgrvtitadkststaymelsslrsedtavyycar 98
                                                                                                                                                                                                                                                             Score 515; DB 12;
Pred. No. 2.00e-32;
13, Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R22358 standard; Protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R38623 standard; Protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 74.8%:
Matches 77; Conservative
                                                                                                                                                                                                                                                             / Match 53.9%;
Local Similarity 74.8%;
nes 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAR-1992.
28-AUG-1991; UO6185.
29-AUG-1990; US-574748.
31-AUG-1990; US-575962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 AA;
N-PSDB; Q89328.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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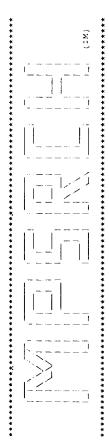
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Example 12, Fage 96, 196pp, English.

A human placental genomic DNA library cloned into the phage vector lambda FIX II was screened with the human VH1 family specific oligonucleotide Q44184. Phage clone lambda 49.8 was isolated and a fib Xbal fragment containing the variable, seyment VH49.8 was subcloned into pNNO3 to generate plasmid pVH49.8 An 800bp region of this insert was sequenced (Q44185) and VH49.8 found to have an open reading frame and inteat splicing and recombination signals, indicating that the gene is functional. Amino acid sequence Q44185 was deduced from the coding sequence; the last 3
                                                                                                                                                                                                                               Transgenic non-human animals contg. immunoglobulin heavy chain trans gene . used to produce useful antibodies by isotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codons before the termination codon have not been translated.
Sequence 117 AA;
sotype switching; H chain variable region.
                                                                                                                                                        (GENP-) GENPHAPM INT INC.
                                                                         17-DEC-1992; U10983.
17-DEC-1991; US-810279.
18-MAR-1992; US-853408.
23-JUN-1992; US-904068.
                                                                                                                                                                            Lonberg N;
                                                                                                                                                                                          WPI: 93-214169/26.
                                                                                                                                                                                                               N-PSDB; Q44185.
                    Homo sapiens.
                                                         24-JUN-1993.
                                                                                                                                                                                                                                                                           switching
                                                                                                                                                                            Kay PM,
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20 gvglv-gsgaevkkpgssvkvsckasggtfssyaiswvrqapggglewmgriipilg-i- 76 1 EVOLLEGSGAEVRKPGSSVKVSCKASGGIFSGHVITWVRQAPGGGLEWMGESTPTFGSAN 60 5, Gaps Query Match 53.9%; Score 515; DB 7; Length 117; Best Local Similarity 74.8%; Pred. No. 2.00e-32; Matches 77; Conservative 13; Mismatches 8; Indels 61 YAQNYAQFFPDPVSJIADESISTSFIELSNIPSDDIAVYYGAR 103 77 -a-myaqkfqgrvtitadkststaymelsslrsedtavyycar 117 CD á

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Page



Pelease 2.10 John P. Collins, Biocomputing Pesearch Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07:31:49 1998; MasPar time 2:19 Seconds 210.908 Million cell updates/sec Run cn:

Tabular output not generated.

(1-132) from US08844215.pep 956 Description: Perfect Score:

. PCYPGFFQQWGQGTLVTVSS 132 1 EVQLLEQSGAEVRKPGSSVK Sequence:

PAM 150 Gap 11 Scoring table:

56402 segs, 5095871 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued libackl 2:51 3:52 4:53 5:54 6:55 7:56 8 pdra0 a pdra1 l0-pdra2 11-pdra3 12-pdra4 13 pdra5 14:pdra6

Mean 28,505; Variance 140 983; scale 0 203 Statistics Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	40.1444448001000000000000000000000000000	
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                                                                                                                                                                                                                                                                                                                                                             METHOD FOR STIMULATING PRODUCTION OF VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION. VACCINATION WITH A B.CELL SUPERANTIGEN AND CONJUG
                                                                                                                                                             61 YAQNYAQKFRDRVSIIADESTSTSFIELSNLRSDDTAVYYCARDPPRYCSAGRCYPG·F· 118
                                                                                                                                                   59 -T-NYAQKFQGRVTITADTSTSTAYMELSSLRSEDTAVYYCARAPG-YGSGGCYRGDYX 115
                                                                                                                            1 EVQLLEQSGAEVRKPGSSVKVSCKASGGTFSGHVITWVRQAPGQGLEWMGESIPIFGSAN 60
                                                                                                           1 QVQLV-QSGAEVKKPGASVKVSCKASGYTFTSYAISWVRQAPGQGLEWMG-WINPYGNGD 58
                                                                                        7; Gaps
                                                                     Length 129;
                                                                                         22; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
                                                                                                                                                                                                                                                   120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Spensley Horn Jubas & Lubitz
1880 Century Park East - Suite 500
                                                                    Score 607, DB 13;
Pred. No. 2.43e-41;
                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: FD-2630
                                                                                                                                                                                                                                                                                                                                Sequence 13, Application PC/TUS9310555 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              Sequence 13, Application PC/TUS9310555.
                                      MOLECULE TYPE: protein
JENCE 129 AA; 13930 MW; 96169 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
                                                                                                                                                                                                                                                                                                                                                  SILVERMAN, GREGG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
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                                                                                                                                                                                                                                                      STANDARD;
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 amino acids
 LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                    63.5%;
ilarity 67.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF INVENTION: THI
NUMBER OF SEQUENCES: 5:
COPRESPONDENCE ADDRESS:
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COMPUTER READARLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Los Angeles
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: pent
                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                      119 FQQWGQGTLVTVSS 132
                              linear
                                                                                                                                                                                          116 FDYWGQGTLVTVSS 129
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                                                                               Local Similarity
es 90; Conser
                                                                                                                                                                                                                                                   PCT-US93-10555-13
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                               TOPOLOGY:
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                                                   SECUENCE
                                                                       Query Match
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METHOD FOR STIMULATING PRODUCTION OF VARIABLE REGION GENE FAMILY RESTRICTED ANTIHODIES
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                                                                                                                                                                                                                                                                                                                           62 AQNYAQKFADRVSIIADESTSTSFIELSNLRSDDIAVYCARDPPPYCSACRCYPGFFQO 121
                                                                                                                                                                                                                                                                                                         57 A-NYAQKEQGRVTITADESTNTAYMELRSLRSDDTAMYYCAKEG--YGDYGRPF-11F--- 109
                                                                                                                                                                                                                                                  2 VOLLEQSGAEVERPGSSVKVSCRASGGTFSGHVITWVPQAPGGGFEWMGFSFPFFGSANY 51
                                                                                                                                                                                                                          1 VHLV-QSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFG--U- 56
                                                                                                                                    Score 559; DR 11: Length 120;
Pred, No. 2.79e-37,
16: Mismatches 14; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10~7
FILING DATE: 20-0~~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS. SO.
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application PC/TUS9310555
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIM
TITLE OF INVENTION: VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FD-2630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application PC/TUS9310555.
                                                         NAME/KEY: Peptide
LOCATION: 1..120
NCE 120 AA; 13008 MW; 78865 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER FOR TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 90067
COMPUTER READABLE FORM:
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                                                                                                                                        Query Match
Best Local Similarity 68.7%;
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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IMMEDIATE SOUPCE.
                                                                                                                                                                                                                                                                                                                                                                                             110 WGQGTLVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                     122 WGOGTLVTVSS 132
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PCT-US93-10555-12
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                   CLONE:
                                         FEATURE:
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                                                                                                       SEQUENCE
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60 AQ----KEQGPVTITTDESTSTAYMEVSSLPSEDTALYYCAPEGPPM-AIN---P--FDY 109
                                                                                                                                                                                                            20; Mismatches 13; Indels 11; Gaps
                                                                                                                                             1 VQLV-QSGAEVKKPGSSVKVTCKASGDTFSSSAISWVRQAPGQGLEWMGGIIPIFGTPNY 59
                                                                                                                                                                    2 VQLLEQSGAEVPKPGSSVKVSCKASGGTFSGHVITWVRQAPGGGLEWMGESIPIFGSANY 51
                                                                                         Score 539; DR 11; Length 120;
Pred No. 1 36e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 529; DP 6; Length 147;
Pred No 9 446-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Polease #1 0, Version #1 25 GIPPENT APPLICATION DATA:
APPLICATION NUMBER: 115/08/217 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION -
APPLICANT: LAKE, PHILIP
APPLICANT: OSTBERG, LAPS
APPLICANT: OSTBERG, LAPS
TITLE OF INVENTION: WARICELLA-ZOSTER VIRUS
TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS
                                                                                                                                                                                                                                                                                                                            147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
JENCE 147 AA; 15801 MW; 123306 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                            PF.T
                                     NAME/KEY: Peptide
LOCALION: 1.120
KCE 120 AA: 12984 MW: 80846 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4. Application US/NR217918
Patent No. 5506132
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08217918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY SELL INCOMMATION:
NAME: Smith, William M
REGISTRATION NYMREP 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFOPMATION:
TELEPHONE: (415) 336-2400
TELEPAX: (415) 326-2422
INFORMATION FOR SEC IT NO. 4.
SEQUENCE CHAPACTEDISTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIRECTOR AVENUE CITY: Palo Alfornia STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 amino acids
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                                                                                         Query Match
Best Local Similarity 66.4%;
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
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 IMMEDIATE SCURCE:
                                                                                                                                                                                                                                                110 WGQGTLVTVSS 120
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               CLONE:
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                                                                 SEQUENCE
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Local Similarity

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                                                                                                                     1 EVOLLEGGSGAEVPRPGSSVKVSCKASGGTFSGHVIIWVPGAPGGGLEWMGESIPIEGSAN 60
                                                              20 QVQLV-QSGAEVKKPGSSVKVSCKASGGTFSNFATSWVFQAPGQGLEWMGRIMPLFVTS- 77
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86; Conservative 20; Mismatches 20; Indels 9; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENEVAL INFURMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
TITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 59.9%, Score ELS, 19 10; Length 102, Local Similarity 74.8%; Fred. No. 1.42e-33; es 77; Conservative 13; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORPESSORES ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COPERATING SYSTEM: PC-DCS/MS-DOS SOFTWARE: PatentIn Pelease #1.0, Version #1.25 CUPREM APPLICATION DATA: APPLICATION NUMBER: PCI/US92/06185 FILING DATE: 19910828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 -A-NYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCAR 102
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MCLECULE TYPE: peptide
JENCE 102 AA; 10940 MW; 55781 CN;
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TELECOMMUNICATION INPOFMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 87654
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: ONG MAINE.
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415-543-5043
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MEDIUM TYPE: Floppy
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PCT-8592-06185-55
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ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                        IBM PC compatible
                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 146
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 55:
                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                   102 amino acids
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                                                                                           oue Market Pl
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                            19920205
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CORRESPONDENCE ADDRESS:
                                                              NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                   COMPUTER PEADABLE FORM MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                              AMINO ACID
         GENERAL INFORMATION:
                                                                                                                                                                                                                                        CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
Patent No. 5633425
                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                          94105
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                                                                                                                                                                         COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVQLLEQSGAEVRKPGSSVKVSCKASGGTFSGHVITWVRQAPGQGLEWMGESIPIFGSAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 515; DB 10; Length 192;
Pred. No. 1.42e-33;
13; Mismatches 8; Indels 5; Gaps
                                                                                                                                                        APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
CORPRESPONDENCES: 152
                                                                                                                                                                                                                        7: William M. Smith
One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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  61 YAQNYAQKFRDRVSIIADESTSTSFIELSNI,RSDDTAVYYCAR 103
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                                              PRT:
                                                                                                                                 Sequence 63, Application PC/TUS9210983 GENERAL INFORMATION:
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JENCE 102 AA; 10940 MW; 55781 CN;
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                                                                                                             Sequence 63, Application PC/TUS9210983
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MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 146
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 63.
SEQUENCE CHARACTERISTICS:
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                                               STANDARD
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AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                19921217
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Aatches 77; Conservative
                                                                                                                                                                                                                                             San Francisco
California
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER
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CLASSIFICATION:
                                                                                                                                                                                                                                                                   USA
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                                              PCT-US92-10983-63
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APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5633425-Human Animals Capable of
TITLE OF INVENTION: Producing Heterologous Antibodies
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APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
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Best Local Similarity 74.8%; Pred. No. 1.42e-33;
Matches 77; Conservative 13; Mismatches 8; Indels
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                                                                                                                                                                               ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/834,539A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 YAQNYAQKERDRVSIIADESTSTSFIELSNLRSDDTAVYYCAR 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 -A-NYAQKEQGEVTITADKSTSTAYMELSSLRSEDTAVYYCAR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
JENCE 102 AA: 10940 MW: 55781 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 63, Application US/U8U53131
Patent No. 5661016
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 63, Application US/08053131.
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVQLLEÇSGAEVEKPGSSVKVSCKASGGTESGHVITWVPÇAFGGGLEWMGESIPIFSSAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                         5, Gapis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application PC/TUS9500067
GENERAL INFORMATION.
APPLICANT. THE SCIPES PESFARCH INSTITUTE
TILLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HERPER
TILLE OF INVENTION: SIMPLEX VIPUS AND METHODS THERPEOR
                                                                                                                                                                                                                                                                                                                                                                                                   Match
Local Similarity 74 9%, Prod No. 1 426-33,
es. 77, Conservative 13; Mismatches 8, Indels
                         ALDER 94103
CAMPUTER FRACABLE FORM.
MEDIUM TYPE: Floppy disk
COMPOTTER: IBM PC compatible
COMPOTTER: IBM PC compatible
COMPOTTER: IBM PC compatible
COMPOTTER: THE PC COMPOTTER: 125
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
FILING DATE: 26-APP-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/910,279
FILING DATE: 17-DEC 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 18-MR-1992
ATTORNEY/AGENT INFORMATION:
NAME: SMITH: WAR-1992
NAME: SMITH: WAR-11992
NAME: WAR-1100 NUMBER: US 07/853,408
PEGISTPATION NUMBER: US 07/853,408
PEGISTPATION NUMBER: US 07/853,408
PEGISTPATION NUMBER: US 07/853,408
PEGISTPATION NUMBER: US 07/853,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 -A-NYAOKFOGRVTITADKSTSTAYMELSSLRSEDTAVYYCAR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YAQNYAQKFRDRVSIIADESTSTSFIELSNLRSDDTAVYYCAR 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSER- Spensley Horn Jubas & Lubitz
STREET - 1880 Century Park East, Suite 500
CITY: Los Angeles
STAIE: California
                                                                                                                                                                                                                                                                   14643-9-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P.F.
                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE, protein
JENCE 102 AA: 10940 MW: 55781 CN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application PC/TUS9500067.
                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHAPACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDAFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
California
: USA
                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY.
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        COUNTRY
                                                                                                                                                                                                                                                                                                                                    LENGIH
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1900
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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60 ---KFQDPLTITADVSTSTAYMQLSGLTYEDTAMYYCAP-VA-YMLEPTVTAGGLDVWGQ 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           f; Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LEQSGAEVKKPGSSVKVSCKASGSSFSSYAINWVPQAPGQGLEWMGGLMPIFFTTNYAQ- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 LEQSGAEVPKPGSSVKVSCKASGGTFSGHVITWVPQAPQGGLEWMGESIPIFGSANYAQN 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application PC/TUS9311612
GENERAL INFORMATION:
APPLICANT: CO, Man Sung
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: L.Selectin
NUMBER OF SEQUENCES: 12
CORRESPONDED ADDRESS:
ADDRESSEE: Townsend and Townsend Khouric and Crew
STREET: Onc Market Plaza. Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 515: DB 13: Length 122: Pred. No. 1.42e-33: 20: Mismatches 21: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IRM PC_COMPATIBLE
OPERATING SYSTEM: PC-DGS/MS-DGS
SOFTWARE: Patentin Release #1.0, Version #1.25
COMPUTER: IBM PC compatible OPERATING SYSTEM: PG-LOGS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                           UMBER PCT/US95/00067
04-JAN-1995
                                                                                                                                                                                                                          FD-3229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Peptide
LOCATION 1.122
NTE 127 AA; 12999 MW; R6642 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application PC/TUS9311612.
                                                                                                                                                                                                                   PEFBENCE/DOCKET NUMBER FD-32
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS.
LENGTH: 122 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                               ATTORNAY AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
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                                                             CURRENT APPLICATION DATA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 63.3%;
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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CLONE: FabHSV 8
                                                                                                         FILING DATE: 04
CLASSIFICATION:
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PCT-US93-11612-8
                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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CURRENT APPLICATION DATA:

US-08-844-215-1.rai

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                                                                                                                                                                                                                                                                                            61 YAQNYAQKFRDRVSTIADESTSTSFIELSNLRSDDTAVXYCARDPPRYCSAGRCYPGFFQ 120
                                                                                                                                                                                                                                               1 QVQLV-QSGAEVKKPGSSVKVSCKASGYTFTSYVMHWVRQAPGQGLEWIG--Y-IYPYND 56
                                                                                                                                                                                                                                                           Score 512; DB 11; Length 121;
Pred. No. 2.54e-33;
24; Mismatches 16; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application PC/TUS9311612
GENEPAL INFORMATION:
GENEPAL INFORMATION:
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: L-Selectin
NUMBER OF SEQUENCES:
CORPESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: TRM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                140 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IS 07/983.946
FILING DATE: 01-DEC-1992
  APPLICATION NUMBER - PCT/US93/11612
                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, william M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                    11823-22
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application PC/TUS9311612
                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 121 AA: 13661 MW; 87993 CN;
                                                                                 REFERENCE/DOCKET NUMBER. 118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                             TELFERAL 415-26-2422
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                           LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                            Match 53.6%;
Local Similarity 61.4%;
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                           110 DWGQGTLVTVSS 121
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                                                                                                                                                                                                                                                                                                                                                                          JT 11
PCT-US93-11612-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                 81;
                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1900
                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                     XXXXXX
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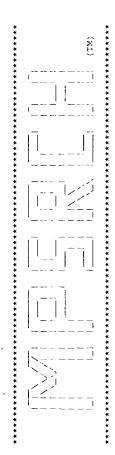
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76 -GTKYNEKFKGRVTIITSDESTNTAYMELSSLRSEDTAVYYCAREE--Y---GN-YVRYFU 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YAQNYAQKFRDRVSIIADESTSTSFIELSNLRSDDTAVYYCARDPPRYCSAGKCYFGFF0 120
                                                                                                                                                                                                                                                                                                                                                                                                               20 QVQLV-QSGAEVKKFGSSVKVSCKASGYTFTSYVMHWVRQAPGGGLEWIG--Y-IYIYND 75
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                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                       24; Mismatches 16; Indels 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/U84/7728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HIMMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                        Score 512; DB 11; Length 140;
Pred. No. 2.54e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOPTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Townsend and Townsend and Crew LLP Two Embarcadero Center, 8th Floor
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-16C-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ns 67/310 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 140 AA, 15650 MW; 117746 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER FEADABLE FORM SISK COMPUTER: IS BY COMPATIBLE COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                        REFERENCE/DOCKET NUMBER: 1182.
TELECOMMUNICATION INFOPMATION:
TELEFAX, 415-326-2400
TELEFAX, 415-326-2422
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08477728
                                            30,223
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PRIOR APPLICATION DATA:
AFFLICATION NUMBER: US 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995
N: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                     NAME: Smith, William M. REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: TWO C. CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 61.4%;
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER-
FILING DATE: 07-JUN
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-477-728-4
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RESULT
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                                                                                                                                                                                                                                                Saps
                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMINISELUSELINS
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                              Query Match 51.2%; Score 489; DB 6; Length 117; Best Local Similarity 70.6%; Pred. No. 2.17e-31; Matches 72, Conservative 16, Mismatches 9, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Enharcadero Center, 8th Floor STRIT: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                 61 YAQNYAQKFRDRVSIIADESTSTSFIELSNLRSDDTAVYYA 102
                                                                                                                                                                                                                                                                                                    60 YAQ----KFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA 97
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/477,728 FILING DATE: 07-JUN-1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94111
COMPUTER PEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC COMPATIEN:
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/08477728
Patent No. 5585089
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/08477728
FILING DATE: 13-FER-1989
                                                                                                                              TOPOLOGY: unknown MOLECULE TYPE: protein HYPOTHETICAL: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 07-JUN-:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                             NAME/KEY: Protein
                                                                                                                       TYPE: amino acid
STPANDEDNESS sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΩS
                                                                                                                                                                                                                                                                                                                                                        US-08-477-728-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1900
                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                           XXXXXX
                                                                                                                                                                                                                                                                                                                                                RESULT
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1 QVQLV-QSGAEVKKPGSSVKVSCKASGGTFSRSAJIWVPQAPGQGLFWMGGTVPMFGPPN 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
15
15
(1)
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OTHER INFORMATION: /note≠ "Eu heavy chain amino acid
OTHER INFORMATION: Sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 489; DB 6; Length 117;
Pred. No. 2.17e-31;
16, Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APFLICANT: SELICK, Harold E. TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNGBOBLINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEFERENCE/DOCKET NUMBER: 11823-002600 TELECOMMUNICATION INFORMATION TELEBHONE: (415) 326-2400 TELEBHONE: (415) 326-2422 INFORMATION FOR SEQ 1D NO: 15 SEQUENCE CHARACTERISTICS:
                                                        FALSA METLICALIA LANGER 100 (7/590,274 FILING DATE: 28-5EP-1990 FILING DATE: 28-5EP-1990 FILING DATE: 28-5EP-1990 FILING DATE: 18-5EP-1989 FILING DATE: 13-FEB-1989 FILING DATE: 28-DEC-1988 ATTORNEY/AGENI INFORMATION NUMBER: 50.233 FEGISTRATION NUMBER: 30,223
    US 07/634,278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P INFORMATION: Sequence "
117 AA; 12472 MW; 77871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/07634278 Patent No. 5530101 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15, Application US/07634278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 379 Lytton Avenue CITY: Palo Alto
                          19-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QUEEN, Cary L.
                                                                                                                                                                                                                                                                                                                                                                                                                   117 amino acids
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APPLICATION NUMBER: 1
FILING DATE: 19-DEC-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 70.6%;
Matches 72; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STFANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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1 QVQLV-QSGAEVKKPGSSVKVSCKASGGTFSRSA11WVPQAPGQGLEWMGGIVPMFGPPN 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Protein
LOCATION: 1.117
OCHER INPORMATION: /note= "Eu heavy chain amino acid
OTHER INFORMATION: sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: QUEEN, Cary L.
APPLICANT: QUEEN, SUNG
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, William P.
APPLICANT: COELTNGH, Kathleen L.
APPLICANT: COELTNGH, Kathleen L.
APPLICANT: SELCK, Aarold E.
APPLICANT: SELCK, Aarold E.
APPLICANT: SELCK, Aarold E.
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 489; DB 6; Length 117;
Pred. No. 2.17e-31;
16; Mismatches 9, Indels
                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 YAQ----KFOGRVTITADESTNTAYMELSSLRSEDIAFYFCA 97
                                                                                                                                                                                                                                                                                                                  11823-002600
                                                                                                                                                                                  APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA: US 07/290,975
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTOPREY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION UNMBER: 30,223
PREPERFENCE
                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
                                                                              UMBER: US/07/634,278
19-DEC-1990
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117 AA: 12472 MW: 77871 CN:
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                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER 110
                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 326-2400
TELEFAX. (415) 326-2422
INFORMATION FOR SEQ ID NO. 15:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                          117 amino acids
                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US.
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 51.2%;
Best Local Similarity 70.6%;
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
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GENERAL INFORMATION:
APPLICANT: QUEEN,
                                                                                                     FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-07-634-278-72
                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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1 QVQLV-QSGAEVKKPGSSVKVSCKASGGTFSFSATIWVKÖAFGGGLEWMGGIVPMFGPPN 59
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CORPESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DFG-1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6U YAQ----KFUGRVIITADESTNIAYMELSSLRSEDIAFYFCA 97
                                                                                                                                                                                                                                                                                                              11823-002600
                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28 SEP-1990
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
JENCE 117 AA; 12472 MW; 77871 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: Tue Feb 24 07:32:05 1998
                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                               TORNEY/AGEN, 111.
                                                                                                                                                                                                                                                                                                                                            TELEFAX. (415) 326-2422
INFORMATION FOR SEQ ID NO: 72:
                        379 Lytton Avenue
                                                                                                                                                                                                                                                                 FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                              117 amino acids
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rest Legal Similarity 70.6%;
Matches 72; Conservative
                                                                             COMPUTER READARLE FORM:
MEDIUM TYPE: Floppy
                                   Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                   94301
                                                                                                                                                                                                                                                                                                                                                                                                                  COPOLOGY:
                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                 LENGIH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Pelease 2 1D John F Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, H K Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Feb 24 07.02/25 1938. Masket time 8.25 Secrible 487.247 Million cell updates/sec Run cr..

Tabular output not generated

>US-08-844-215-1 (1-132) from US08944215.pep 956 1 EVQLLEQSGAEVPKPGSSVK... Description: Perfect Score:

Sequence:

Scoring table:

PCYPGFFQQWGQGTLVTVSS 132

95051 seqs, 30469580 residues PAM 150 Gap 11 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing.

Database:

1:annl 2:ann2 3:ann3 4:ann4 5:unann1 5:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann9 14:unann10 15:unann11 16:unann12 17:unenc

Mean 41.620; Variance 105.958; scale 0 393 Statistics: Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.		216-7	.540-7	.57e-7	270-7	100-5	8.80e-69	.90e-5	.14e-6	.11e-6	ن - ن	9-a	10-6	9-a	9-06	.726-5	640-6	.64e-5	2 420-64	.42e-6
Description	heary chain V r	heavy chain V r	Iq heavy chain V-1 r	heavy chain V re	Ig heavy chain V-1 r	anti-PR2 crythrocyte	q heavy chain V	heavy chain V	g heary chain V	q heary chain V	a heavy chain V	Iq heavy chain V req	g heavy chain V	heavy chain V-	g mu cha	q heavy cha	z V ahain V z	heavy chain V r	Is heary chain V res	g heavy chain V-1
ID	PHOSE	560	A33548	395	B33548	C.	10	10	10	55	LC.	A49590	o.	7	8	DHOOKU	<u>u</u>	95		25.4
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Query Match Length	u. Ci	00 C1	129	127	126	160	C)	135	132	129	116	121	135	133	627	136	311	122	011	CI CI
Query Match	ι.	-4		60.4	0	σ	on	ά	ထ	7	7	7	7	7	۲.	9.	G)	ω,	56.3	Ġ
Score	ς (2)	α	~	7	575	vc.	9	O	S	S	4	₹.	マ	4	4	4	4	4	538	m
Result No.	-1	CI	m	4	2	9	7	ω	σ	10	11	12	13	14	15	16	17	18	61	C1

3.49e-64 2.49e-64	3-36F.	.23e-6	.23e-6	10e-6	30-	.51e-6	.04e-6	040-6	15e-6	.4le-6	93e-5	110-5	4 6.0 - F	.11e.5	.98e-5	.29e-5	.660-5	9 9 10 10 10 10 10 10 10 10 10 10 10 10 10	.13e-5	320-5	2e - 5	.02e-5	-906
chain chain	g heavy chain V-	g heavy chain VI	g heavy chain v	J heavy chain V	g heavy chain V	g heavy chain pr	g heavy chain Vl	g heavy chain V	g heavy chain V	g heavy chain v	q heavy chain v	g heavy chain V	3 heavy chain V	g heavy chain V	g heavy chain V	g heavy chain V-	g heavy chain V	V niedry yvedin V	q heavy chain v	q heavy chain V-	q heavy chain V	q heavy chain V	g heavy chain V
7 S26915 7 S31698	5441	S246	8441	PH15	B495	B322	8464	5463	C49	8213	PHOR	\$196	2362	2678	PH16	GIHO	A324	100 M	8316	A305	PH16	F495	I441
110	12	CT)	H		C	C) E1	σ	런	T	73	σ	12	E.	-1	10	r 1	14	, ,	II	œ,	10	텀	12
537 56.	37 56.	35 56.	35 56.	3.1	27 55.	18 54.	15 CB	15 53.	13 53.	10 53.	05 52.	03 52.	99 52	94 51.	90 51.	89	87 50.	100 100	83 50.	81 50.	75 49.	75 49.	74 49.
C3 C4 E4 C3	23	4	5.5	٧.	27	C1 0)	os Ci	30	31	32	33	34	3,5	36	37	<u>ه</u>	39	C.	41	C1	43	44	45

ALIGNMENTS

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#title Developmentally restricted immunoglobulin heavy chain variable region gene expressed at high frequency in chronic lymphocytic leukemia.
                                                                                                                                                                                                                                                                                                           *superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kipps, T J , Tombave, E , Pratt, L F , Duffy, S., Chon, P.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 yaq----kfqgrvtitadkststaymelsslrsedtavyycarggnydyiwgsyrsndaf 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 qvqlv-qsgaevkkpgssvkvsckasggtfssyaiswvrqapggglewmggiipifgtan 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVOLLEOSGAEVRKPGSSVKVSCKASGGTFSGHVITWVRQAPGQGLEWMGESIPIFGSAN 60
                  PH0952 #type fragment
Ig heavy chain V region (6+ CLL-SMI) - human (fragment)
#formal_name Homo sapiens #common_name man
17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain V-I region (NEI) - human
#formal_name Homo sapiens #common_name man
17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                       immunoglobulin homology #label IMM\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            complementarity-determining 1/
                                                                                                                                                                                                                                                                                                                                                                                                                              framework 2\
complementarity-determining 2\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #region complementarity-determining 3
#length 128 #checksum 3537
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                                                                                                                                                                                                                                                     nucleic acid sequence not shown
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Pred. No. 1.21e-71;
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#region complementari
#region framework 3\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *type complete
                                                                                                                                                                                                                                                                                                                                                                      #region framework 1\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -129 ##label KIF
                                                                                                                                                                                                                                                                                        1-128 ##label MAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 61.1%;
Best Local Similarity 67.9%;
Matches 91; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carson, D.A.
                                                                                            16-Aug-1996
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                                                                                                                                                                                                                                                                                                                                                                                           #domain
                                                                                                                                                                                                                                                                                                                                                                                                            *region
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*superfamily immunoglobulin V region; immunoglobulin homology
                  *superfamily immunoglobulin V region; immunoglobulin homolody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal Texp Med (1992) 175:988-991
#fills Evidence for somatic selection of natural autoantibodies.
#cross.references MID:92202880
#accession PH0955
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Pred No. 7.54e-71;
16; Mismatches 19; Indels
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Pred. No. 1.57e-70;
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Best Local Similarity 68.7%;
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                                                                                                                                                                     *Journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:5913-5917
#title Developmentally restricted immunoglobulin neavy chain variable region gene expressed at high frequency in chronic lymphocytic leukemia.
#cross-references MUID:89345575
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The antibody is one of the cold agglutinins that preferentially bind red blood cell membrane antigens at low temperature, causing cold agglutinin disease (CAD).

ITON #superfamily immunoglobulin V region; immunoglobulin homology authoraty; hemagalutinin
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J. Exp. Med. (1949) 149-1611-1643
Pelationship of variable region genes expressed by a human B
cell lymphoma secreting pathologic anti-Pr-2 erythrocyte
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31-Mar-1990 #sequence_revision_31-Mar-1990 #text_change
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                                                                                                                                                        Kipps, T.J., Iomhave, E., Pratt, L.F., Buffy, S.,
Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. (1989) 86:5913-5917
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#cross-references MUID:89235583
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J. Exp. Med. (1992) 175:983-991
Evidence for somatic selection of natural autoentibudies.
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Ig heavy chain V region (G6+ T-142) - human (fragment)
#formal_name Homo saplens #common_name man
17-Aprr1993 #sequence_ceristion if Aprr1993 #text_phange
16-Aug-1996
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Pred. No. 8.80e-59;
14; Mismatches 11; Indels 12; Gaps
                    #domain immunoglobulin homology #label IMM\
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Pred No. 6 10e-69,
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#length 120 #checksum 5559
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#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
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                                                                                                                                                                                     #authors Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross_references_MUID:92202880
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Pred. No. 7.90e-68;
16; Mismatches 8; Indels 8; Gaps
Iq heavy chain V region (G6+ CLL-SIC) - human (fragment)
#formal_name Homo sapiens #commou_name man
17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
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Griffiths, A.D.: Malmqvist, M.: Marks, J.D.: Hye, J.M.:
Embleton, M.J.; McCafferty, J.: Raier, M.; Holliqer, K.P.:
Gorick, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.R.: Winter,
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Embleton, M.J.; McCafferty, J.; Baier, M.; Holliqer, K.P.;
Gorick, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.R.; Winter,
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Human anti-self antibodies with high specificity from phage
display libraries.
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                                                 60 yaq----kfqgrvtltadeststaymelsslrsedtavyycarphasiddfwsqyypnyy 115
                                                                                                61 YAQNYAQKFRDRVSIIADESTSTSFIELSNLRSDDTAVYYCARDPPRYCSA-GRCYPGFF 119
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03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
1 EVQELEQSGAEVRKPGSSVKVSCKASGGTFSGHVJTWVRQAPGQGLEWMGESIPIFGSAN 60
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03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
16-Aug-1996
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                                                                                                                                                                                                                                                                                                      836260 #type fragment
Ig heavy chain V region (clone alpha-CEA4-8A) · human
(fragment)
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1g heavy chain V region (clone alpha-TNF-E7) - human
(fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 551; DB 7; Length 129;
Pred. No. 2.11e-66;
26; Mismatches 18; Indels
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Best Local Similarity 61.9%;
Matches 83; Conservative
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CLASSIFICATION
KEYWORDS
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  ACCESSIONS
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain V region (ACHSV1, clone 15) - human (fragment) #formal_name Home sapiens #commor_name man 06-oct-1994 #seguence_revision 18-Nav-1994 #text_change
                 ##residues 1-116 ##label GRI
##cross-references EMB12.18841
FFCALION *superfamily immunoglobulin V region; immunoglobulin homology
DS
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##molecule_type nucleic acid
##residues 1-121 ##label BUP
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                                                                                                                                                                                                                                                                                        20; Mismatches 19; Indels 6; Gaps
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                                                                                                                                                                                                                           6; Gaps
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Ig heavy chain V region - human
#formal_name Homo sapiens #common_name man
27.Jan-1995 #sequence_revision 27.Jan-1995 #text_change
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#title Recombinant human Fab to glycoprotein D neutralizes
infectivity and prevents cell to-cell transmission
hcross-references MUID:94105168
                                                                                                                         #domain immunoglobulin homology #label IMM
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                                                                                                                                               Best Local Similarity 74.3%; Score 549; DB 7; Length 116; Matches 81; Conservative ...
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Pred No. 1.31e-65;
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##experimental_source bone marrow lymphorytes
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Best Local Similarity 64.3%;
Matches 81; Conservative
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##molecule_type mRNA
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#fitle bevelopmentally restricted immunoglobulin heavy chain variable region gene expressed at high frequency in chronic lymphocytic leukemia.
#cross references MUID:89345575
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FICALIGN #superfamily immunosatiobalin V region; immunoglobalin homology
DS heterotetramer; immunoglobalin
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545390
Figini, M.; Marks, J.D.; Winter, G.: Griffiths, A.D.
J. Moi. Biol. (1994) 239:58-78
In Vitro assembly of repertoires of antibody chains on the
surface of phage by renaturation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 546; DB 7; Length 132;
Pred No. 1.31e-65;
20; Mismatches 18; Indels 10; Gaps
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#formal_name Homo sapiens #common_name man
17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
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compared with conceptual translation
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                                                                                                                                                                                                                                                    1-132 ##label FIG
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Local Similarity 65.0%;
es 89; Conservative
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#domain signal sequence #status predicted #label SIG\
#product Ig mu chain #status predicted #label MAT\
#domain immunoglobulin homology #label IMM
#length 627 #molecular-weight 68510 #checksum 8581
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Ig mu chain precursor, membrane-bound (clone 201) - human
#formal_name Homo sapiens #common_name man
31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 qyqlv-qsgaevkkpgssvkvsckasggtfssyaiswyrqapggglewmggiipifgtan 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 57.0%; Score 545; DB 7; Length 627;
Best Local Similarity 66.4%; Pred. No. 1.89e-65;
Matches 93; Conservative 20; Mismatches 12; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                        immunoglobulin; membrane protein
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118 ---FF-QO-WGGGTLVTVSS 132
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S14683; S08047
                                                                                                                                                                                                                                                                                              ##molecule_type mRNA
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                                                                               RESULT 15
                                                                                                                                                                       ACCESSIONS
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16-627
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ORGANISM
                                                                                                                                                                                          REFERENCE
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Ċ S	ore or the	score or the result being printed	printed,	X	[7]				
į.	al score d	otal score distribution.		er i	DISULFIDE BOND	SOND.			
				KX	MEDLINE; /106402/	.06402/.			
S				RA	GALL W.E., EDELMAN G.M.;	EDELMAN G			
				RL	BIOCHEMISTE	Y 9:3188-3	BIOCHEMISTRY 9:3188-3196(1970).		
				ij.	-!- THE SEC	UENCE OF 1	THE GAMMA-1	C PEG	-!- THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS MY!
	Description	ion	Pred No.	ט	ALSO BE	ALSO REEN DETERMINED	INED.		
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3	IG HEAVY	CHAIN V-I FE	1 226.81	E.G.	HSSF, P01810, 1FVB	.0, 1FVB.			
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E:		CHAIN V PEGI	7 199-58	£.	DISTLFIE	CI	96		
Z	IG HEAVY	CHAIN PPECUP	3 300-67	Ц	NON TER		117		
[i]	IG HEAVY	CHAIN PPECUP	1 900-65	C.	SECTENCE	AA	12472 MW	FCROET	CCCDAD ULTERBOODS
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z	IG HEAVY	CHAIN V-I RE	3.000-63	n.č	Query Match	.,	51.2%; Sco	re 189,	Score 489, DB 5; Lena'
Ŋ	IG HEAVY	CHAIN V-I PE	4.976-53	Be	Best Local Similarity				Fred. Nc. 1.22e-81;
Z	IG HEAVY	CHAIN V-III	4.97e-63	Ma	Matches 72;			16, Mismatches	tches 9, I
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z	IG HEAVY	CHAIN V-I RE	3 210-58	40	1 EVOLLI	USGAEVRKP	SSVKVSCKAS	GGIFSG	EVOLLEUSGAEVRKPGSSVKVSCKASGGTFSGHVITWVRGAPGGGL
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HV51_MOUSE HV06_MOUSE HV07_MOUSE

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                                                                HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRAIA; TETRAPODA: MAMMALIA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG HEAVY CHAÎN PRECHRSOP V-I PEGION (V35).
HOMO SAPIENS (HUMAN)
ETKAPYOTA: METAZOA: CHORDATA: VEKIEKKATA: TETPAPODA: MAMMALIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MATSUDA F., LEE K.H., NAKAI S., SATO T., KODAIRA M., ZONG S.Q. OHNO H., FUKUHARA S., HONJO T.;
EMBO J. 7:1047-1051(1988).
                                                                                                                                                                                                                                                                           IG HEAVY CHAIN V REGION (HG3)
                                                                                                                                                                                                                                                                                                                                      Ouery Match 46.5%; Score 445; DB 5; Length 117; Best Local Similarity 66.0%; Pred. No. 7.54e-72; Matches 68; Conservative 17; Mismatches 13; Indels
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46 0%; Score 440; DR 5; Length 117;
Best Local Similarity 66.0%; Pred. No. 9.65e-71;
Matches 68; Conservative 13; Mismatches 17; Indels
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                                                                                                                             SEQUENCE FROM N A BEDLINE, BAILAGOB N A BEDLINE, BAILAGOB D.; BECHAUL G., RAM D., GLAZER L., ZAKUT K., GIVOL D.; PROC. NATL ACAD SCI. U S A 80.855-859(1983) EMEL; J00240; G553411; -.. PIR; AQ2024; HVH9HG HSSP; PO1810; IFVB.
                                                                                                                                                                                                                                                                                                           117 AA; 12946 MW; BCCBB1DB CRC32;
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20 117 IG HEAVY CHAIN V
117 117
117 AA; 13009 MW: FAAGGDI GFG32,
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1996 (PEL. 34, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN PHECHESOP V-1 PEGION (HG3)
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01-NOV-1991 (REL. 20, LAST SEQUENCE HPDATE)
01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
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CAPPA J D. NISCHOFF A.;
J. IMMUNOL. 123:279-284(1979).
-1- ANTIBORY ISOLATED PROM TEN MICE WAS EXCLUSIVELY OF THE 1003
SUBCLASS. THERE WAS NO HETHOGENEITY IN THE HEAVY CHAIN V REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Indels '; Caps
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KNIEN T.H., MUZGAARCH.V., HOGGHTON M., DEPRYSHIPE P.P., VINEY J.,
BELL L.O., SOLLD H.J.;
PROC. NATL ACAD, SCI U.S.A. 79+6661-6668(1982).
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INI IMMEDIATE PYPERSENSITYIYIY MODERN CONCEPTS AND DEVELORDMENTS.

PACH M K., ED., PR 1-34, MAPCEL DEKKEP, NEW YOFF, (1078).

-!- THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.

PER, ACQUOSES EMUND.

HSSP, POIGOS: IPGV.

IMMEDIATIONAL JEGV.
                                                                                                                                                                                           EUKARYOTA, METAZOA: CHORDATA; VERTEBRATA; TETRAPODA: MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA: CHOPPATA, VERTEBRATA: TETRAPODA: MAMMALIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.7%; Score 427; DB 5; Length 114; 63.3%; Pred. No. 7.19e-68; vative 22; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 yp-nyaqkfqgrvtitadestntaymelsslrsedtavyfcavrvisry 104
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21-JUL-1986 (PEL, 01, LAST SEQUENCE UPDATE)
01-JUL-1986 (PEL, 16, LAST ANDITION UPDATE)
IG HEAVY CHAIN PRECURSOR V-I REGION (ND) (FRAGMENTS).
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H -> HI (IN REF. 2).

VG -> GV (IN REF. 2).

MISSING (IN REF. 2).
                                            21-JUL-1996 (PEL. 01, CPEATED)
21-JUL-1986 (FEL. 01, LAST SEGUENCE UPDATE)
21-JUL-1986 (PEL. 01, LAST SEGUENCE UPDATE)
11. JUL-1986 (PEL. 01, LAST ANNOTATION UPDATE)
MIS MISCULUS (MOUSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMUNOGLOBULIN V REGIÓN; ANTIARSONATE ANTIRODY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 AA; 12555 MW; 1A027F1D CRC32;
114 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 AA.
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es 69, Conservative
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STANDARD;
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143
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HSSP; P01772; 1FGV.
                                                                                                                                                                                                                      ETTHERIA; PODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUTHERIA; PRIMATES.
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HVlc_HUMAN
                                                                                                                                                                                                                                                                                                           STPAIN-A/J;
HV00_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
SEQUENCE
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                       P01741;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                            73 -t-nyapríggrytmtrdasfstaymdlrslrsddsavfycaksdpfwsdyynfdysytl 130
                                                                                                                                                                                                                                                                                                                                                                                                                                 61 YACHYACKEPURVSIIAN-ESISISPIELSNI PSPCIAVYYCAPUPPHYTSA-GPCYPGFF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 yi-nynekfkgkttltvdkssstaymqlrsltsedsavyfear--shyyg-gs-y-df-d 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 gtglvrgsgaevrkpgasvrvsckasgytfidsyihwirgapghglewvg-winp-nsgg 72
                                                                                                                                                                                                                                                        indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 evgl.ggsgaelvragssvkmsckasgytftsygin#vkgrpggglewig.yinp.gng. 75
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                                                                                                                                             Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCIENCE 216:309-311(1982).
EMBL. 101493: G195007: -
PIP: AQ2028: HVNSC7
HSSP: P01789: FFAR.
IMMUNGSLORULIN V PESTON: ANIARSONATE ANTIRODY; HYBFITOMA; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL'1996 (PEL. 01, CPEATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V REGION (36-65).
MUS MUSCULUS (MOUSE),
EUKHPYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HV02_MOUSE STANDAPD: PPT: 140 AA
P01746;
21-JJ1-1996 (PEL OL, CREATED)
21-JJ1-1996 (FEL OL, CREATED)
21-JJ1-1996 (FEL OL, LAST SEQUENCE UPDATE)
C1-CT-1996 (REL 34, LAST ANNOTATION UPDATE)
IGHEAVY CHAIN PRECURSOR V REGION (93G7).
BUTS MUSCULUS (MOUSE).
EUKAPYOTA: METAGOA: CHOFDATA: VEFTERFATA, TETPAPODA, MAMMALIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IG HEAVY CHAIN V REGION (93G7).
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                                                             Score 424, DR F. Length 143,
Pred. No. 3.30e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMS I., PARRITTS I H . ESTESS P . SLAUGHTER C ., THICKER P
                                                                                                                                         24; Mismatches 33; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30, Mismatches 23,
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Pred No 1.90e-65;
143 AA; 16051 MW; 6D605E13 CPC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 AA; 15514 MW; 0700D5C8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPT;
                                                                    Query Match
Best Local Similarity 52.6%:
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 51.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 dvwgggttvtvss 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 COWGGGTLVIVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 ywddatpityss 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE: P2152919
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HV03_M0USE
P01747;
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SEQUENCE
   SEQUENCE
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Sporte 412; DR 5: Longth 120;
Pred. No. 1.44e-64;
32; Mismatches 22; Indels 11; Gaps 10;
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m
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MEDLIND, 8131846.

SIENEVUTE M. DEPERMINA .

SIENEVUTE M. DEPERMINA .

EUR J. CATHERIEN A .

EUR J. LAMINGL 12 1023-1932(1992).

- FPOM ARALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES THAT HYBRICTE TO THIS ONE. THE AUTHORS OF MILLIE THAT ALL OF THE SAME J SEGMENT, JH2.

PLSS A02028 HVMSG7.

IMMUNOSLOBULIN V PRGION: ANTIAPSONATE ANTIBODY: HYBRIDOMA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLLEQSGAEVRKPGSSVKVSCKASGGTFSGHVITWVRQAPGQGLEWMGESIPIFGSAN 60
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ANDREWS D.W., CAPRA J.D.;
BIOCHEMSTRY 20:5822-5830(1981).
-!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOMO SAPTENS (HUMAN).
EUKAPYOTA, METAZOA: CHOPDATA: VFFTERPATA; TETRAPODA: MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Personal 124
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Pred No 3 006-63;
                                                                                                                                                                                                                                                      120 120
120 AA, 33307 MW, RRARGGA1 GRG32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 AA; 13732 MW; C1E9663D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (PEL. 01, CPEATED)
21-JUL-1986 (PEL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (PEL. 01, LAST ANNOTATION UPDATE)
1G HEAVY CHAIN V-I PEGION (SIE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Mismatches
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                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.4%;
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 50 8%;
ses 67, Conservative
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HSSF; F01857; 2FGW.
IMMUNGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDAPP:
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                                                                                                                                                                                                                                                                                                                                        1 qvqlv-qsqaevkkpqssarlsckvsqddfntydihwvrqapgrglewm--av-vhpsdd 56
                                                                                                                                                                                                                                                                                                                                                              1 EVQLLEQSGAFVRKPGSSVKVSCKASGGIFSGHVITWVRQAPGGGLEWMGESIPIFGSAN 60
                                                                    HOMO SAPIENS (HUMAN).
EURARYOTA: METAZOA; CHOPDATA; VEPTERPATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IG HEAVY CHAÎN V-III REGION (KOL).
HOMO SAPIENS (HUMAN).
EUKARYOTA: METRAZOA: CHOPPATA; VEPTERPATA: TEIPAPODA; MAMMALIA:
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                     Score 405, DB 5; Length 125,
Pred, No. 4,97e-53;
                                                                                                                                                                                                                                                                                                                28; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYPROLIDONE CARROXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE, 83289131.
SCHMIDT W.E., JUNG H.-D., PALM W., HILSCHMANN N.;
HOPPE-SEYLER'S Z. PHYSIGL, CHEM 364-713-747(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE, 81072295.

MARQUART M., DEISRHOFER J., HUBER R., PALM W.,

J MOL RIOL. 141.359-391(1980).

PIR: A02055; G1HUKL.

PDB: 2F84; 12-3UL-89.

PROM: 2162: 12-3UL-89.

IMMUNOSIORALIN V PEGION: 3D-STPUGTUPE.
                                                                                                                                                                                                                                                                 13579 MW; 67450023 CRC32;
                    01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-I PEGION (MOT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P01772;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01. LAST SEQUENCE UPDATE)
01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                      V SEGMENT.
D SEGMENT.
J SEGMENT.
BY SIMILARITY.
                                                                                                                               MEDLINE; 86203277

KOJINA M., KOIDE I., UDANI S., ONO T.;

MOL. IMMUNDL, 23.169-174(1986).

PIR, A02025, HVUMO.

HSSP, P01772; 8PAB.

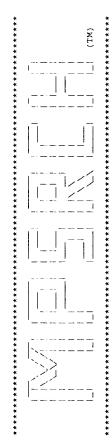
IMMUNOGLOBULIN V REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-PAY CPYSTALLOGPAPHY (1 9 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 47 v...
62; Conservative
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD
                                                                                                                                                                                                      98
107
125
96
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126
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15
25
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22
125
125 AA;
                                                                                             EUTHERIA; PRIMATES
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HV1F_HUMAN
P06326:
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SEQUENCE
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                                                                                                                                                                                                                                                                       1 qvqlve-sgggvvqpgrslrlscsssgfifssyamywvrqappdkqlewv--ai-iwddqs 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 eagl-ggsgaelvrpgtsvkisckaagytftnywiawvkerpghalewigd---iyhaag 56
                                                                                                                                                                                                                                                33; Mismatches 31; Indels 8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA; TETRAPODA: MAMMALIA:
EUTHERIA: RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZAKUT R., COHEN J., GIVOL D.;
NUCLEIC ACIDS RES. 8:4839-4840(1980).
--- THIS SEQUENCE WAS IPANSLATED FROM AN MPNA ISOLATED FROM A MYELOWA HAT SECRETES 1632B.
PIP: A02.027: GVMS11.
HSSP; P01810; 1MFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 41.2%, Scure 394, EB 5, Evneth 121; Local Similarity 46.2%; Pred. No. 1.27e-60; es 51; Conservative 38; Mismatches 22; Indels 1
                                                                                                                                                                                                                           Length 126;
                                                                                                                                                                                                                          Score 405; DB 5; 1 Pred. No. 4.97e-63;
                                                                                                                                                                                                   13718 MW; 14F328CF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
121 AA; 13135 MW; DARFORGO ORC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
13-AUG-1987 (REL. 05, LAST ANNOTATION UPDATE)
1G HEAVY CHAIN V PEGION (MPC 11);
                                                                                                                                                                                                                                                                                                                                                                                                                                          121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZAKUT R., COHEN J., GIVOL D.;
NUCLEIC ACIDS RES. 8:3591-3601(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                        Query Match 42.4%;
Best Local Similarity 45.9%;
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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NON_TER 121 121
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                                                                                                                                                                             113
120
126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE, 81053741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUS MUSCULUS
EUKARYOTA; ME
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YAQNYAQKERDRVSILALESISISPIFISNIPSELTAVYYYARLAPPYGSAGPZYPGFFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 gyelve-saggyvarparslatsaasyftisabyamkarapppykylevva-visybatak 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29; Mismatches 29; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6;
MEDLINE: 81234548.
BOTHWELL A.L.M., PASKIND M., PETH M., IMANISHI-KAPI T., PAJEWSKY K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -0- THIS GERMINE GENERAL BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCORE V PRSTONS OF NPR ANTIHORIES.

EMBL, JOOSSE, GSS44035; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEHWAN D.W., PUTNAM F.W.;
PROC. NATL. ACAD. SCI. U.S.A. 77-3239-3243(1980).
-!- THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A PATIENT WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (PEL- O1, CPEATED)
21-JUL-1986 (PEL- O1, LAST SPWHENCE UPCATE)
01-OCT-1996 (PEL- 34, LAST ANNOTATION UPDATE)
MUS PROV CHAIN PECHPSON V PETITON (?)
MUS MUSCULUS (MOUSE).
EUKARYQIA METADOA, CHOEDATA, TETRAFODA, MAMMALIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN).
EUKARNOTA, METAZOA, CHIEDATA, VERIEBEATA, TETRAFODA, MAMMALIA,
EUTHERIA: PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 394; DB 5; 1
Pred. No. 1.27e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 122
122 AA; 13558 MW; 4AF2E3D9 CPC?2;
                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
11-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN V-III REGION (CAM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 41.2%;
Local Similarity 48.5%;
les 64; Conservative
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HSSP: P01607; 2FGW.
IMMUNOGLOBULIN V REGION.
MOD. PFS. 1
                                                                                                                                                                                                                                                                                           STANDARD
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CELL 24 625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MACROGLOBULINEMIA.
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                                                                      110 Swgggttltvss 121
                                                                                                                                             121 QWGQCTLVTVSS 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A02031; HVMS3
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                                                                                                                                                                                                                                                                                   HV3G_HUMAN
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SEQUENCE
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Query Match
40.1%; Score 383; DB 5; Length 124;
Best Local Similarity 52.6%; Pred. No. 3.21c-58;
Matches 70; Conservative 24; Mismatches 27; Indels 12; Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (n)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 qvql-qqpgaelvrpgssvklsckasgytftsywmdwvkqrpgqglewign---iypsds 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVILLEGSSAEVPKFGSSVKVSCKASGGTFSGHVJTWVPQAPGQGLEWMGESIPIFGSAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE.
MEDLINE: 82046599.
ANDREWS D.W., CAPPA T.D.;
RICCHEMISTRY 20.5822-5829(1981).
-!-TRIS CHAIN WAS ISOLAIER FROM AN ISM WITH ANTI-GAMMA GLOBOLIN
ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMO SAPIENS (HUMAN).
EUKARYOTA, METAZOA, CHORDATA, VEFTERFATA, TFTFAFODA, MAMMALIA;
ETTHERIA; PPIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUS MUSCULUS (MOUSE).
EUKAPYOTA, METARGA, CHGEDATA, VERTERRATA, TETRAPODA; MAMMALIA:
EUTHERIA; RODENTIA.
                                                 COMPLEMENTARITY-DETERMINING 1. FRAMEWORK 2.
                                                                                                                                       COMPLEMENTARITY-DETERMINING 2.
                                                                                                                                                                                                                                                                                                                                                                                          40 2%; Score 384; DB 5; Length 117; 53 4%; Pred No. 1 94e-58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28; Mismatches 15; Indels
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49 FPAMEWOPK 1.
54 COMPLEMENTARITY-DETH
68 COMPLEMENTARITY-DETH
117 FRAMEWORK 3.
117 BY SIMILARITY.
118 BY SIMILARITY.
119 6 WW. OFICEFORD CPC32;
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21-501-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-501-1986 (REL. 01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 15
EV13_MCUSE STANDARD. PRT, 117 AA.
P01757.
201767.
21.7UL-1986 (PRL 01, CPEATED)
21.7UL-1986 (PRL 01, LAST SEQUENCE UPDATE)
01.NOV-1991 (REL 20, LAST ANNOTATION UPDATE)
1G HRAVY CHAIN V PRGTON (JSS8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 AA
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Rost Local Similarity 53 4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDAPD;
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HSSP; P01607; 1FGV.
IMMUNOSLORULIN V PEGION
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50
50
69
86
117
117 AA:
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NON_TER
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NON_TER
             F-PMAIN
DOMAIN
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                                                                                                   DOMAIN
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Release 2.10 John F. Collins, Riocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Tue Peb 24 07:05-52 1998; MasPar time 6.99 Seconds 252.448 Million cell updates/sec Pun on-

not generated. Tabular output >US-08-844-215-2

(1-127) from US08844215.pep 931 Description: Perfect Score:

EVQLLEQSGAEVKKPGSSVK.......HTMGYYFDYWGQGTLVTVSS 127

PAM 150 Gap 11 Scoring table:

Sequence:

111726 segs, 13889129 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq30 Database:

i.part1 2.part2 3.part3 4.part4 5.part5 6.part6 7.part7
8.part8 9.part9 10.part10 11.part11 2.part12 13.part13 11.part14 11.part14 15.part15 16.part16 17.part17 18.part18 19.part19 20.part20 21.part21 22.part12 23.part23

Mean 30.758; Variance 161.149; scale 0.191 Statistics: Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
П	616	9	147	-1	R55019	93KA9 anti-Varicella	1.270-38
CI	613	ι. (1)	C 1	C3	W19888	CEA-specific antibody	
٣	610	u u V	4.8	ĸ,	F24442	Sequence of antibody	3. 4.4
4	(1 ()		L 1	Ċ,	wlจลล	CEA-specific antibody	1.650-37
'n	601	64.6	123		W19886	CEA-specific antibody	1.980-37
9	009	64.4	123	C1	W19881	-specific anti	2.37e-37
7	597	₹.	123		W19887	CEA-specific antibody	4.10e-37
œ	519	52.2	C1	œ,	F54796	SpA-reactive IgM heav	1 100-35
σ	576	61.9	475	ψ٠	531033	Antibody D heavy chai	1.906-35
10	574	Н	120	σ	P54795	SpA-reactive 19% heav	2.740-35
11	572	61.4	36	-	R72068	DF10 VH region.	3.940-35
12	572	61.4	249	14	P77610	Himanised 501.1 VH +	3.940-35
13	565	ο.	122		R76964	HSV-neutralising anti	1.410-34
14	561	60.3	4	⊣	R77615	Humanised 5G1.1 VH +	2.936-34
15	558	o.	11.9	C 1	W12536	Anti-melanema antibod	5.050-34
16	558	9	4	C1	W21847	Humanised heavy chain	5.06e-34
17	554	59.5	248	1	R77616	Humanised CDR-grafted	1.05e-33
18	550	6	ω σ.	e 1	205	HV1253 VH region.	2.170.33
19	550	ς. Γ'	11.7	7	F38623		2.176-33
្ន	O IO	G. U.	1:7	4	00 to	Protein encoded by th	2.17e-33

Saps Saps

Query Match 66.2%; Score (16; DB 12; Length 147; Bost Local Similarity 66.7%; Prod. No. 1.278-38; Matches 86; Conservative 19; Mismatches 12; Indols 1

.17e-3	2.61e-33	.13e-3	13e-3	13e-3	.50e-3	.50e-3	.78e-3	.78e-3	346-3	.34e-3	.33e-3	.33e-3	336-3	336-3	.90c-3	.90e-3	90e-3	27e-3	.71e-3	71e-3	.71e-3	71e-3	.71e-3	.05e-3
aqmest vh49.8	hai	sed mouse DEG-	Tonal antibody	I	artibody BT	Heavy chain variable	400	Heavy chain variable	ised	Humanised heavy chain	Heavy chain variable	ised CD	>	-5A8 humanised	ated humanised he	==	sed anti	PHB VH	noclonal ant	1748PHA VH 1	PB1.3/Humanised heavy	1748RHC VH regio	.3/Humanised hea	Heavy chain VHIS 4 fr
9	W21849	787	6.0	10	350	118	110	.7	5.7	185	019	760	75	SRO	793	126	123	267	561	257	369	25.5	R43689	G.
C1	<u>C1</u>	7	σ	c	ن 1	6	C 1	'n	Ŋ	23	σ	14	1.4	٠.	∞	12	C 1	Ξ	თ	11	ထ	디	∞	4
117	140	121	C 1	140	C.1	4	Т	\vdash	C 1	₹	4	4	4	vc	CA	4	77	α,	< 1	ペ.	6.3	ζ,	139	-1
σ,	59.0	a)	α	α	ω.	8	a)	8	8	ω.	7	7	7	7	7	7	7	Ġ	ė.	Ġ	9	9	ė.	œ.
L)	549	₹.	**	<*	7	4	7	ಶ	7	4	3	3	ς,	ζ.	3	3	(2)	3	(1	(1	CI	C1	2	C 1
21	G	£.	ri Ci	ርነ ሆ.	52	27	8 2	62	30	31	32	33	3.4	ር የ	36	3.7	38	39	40	 **	4	43	44	ti i

ALIGNMENTS

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PUBLISHED 1994; U08241.

22-JUI-1994; U08241.

28 -JUI-1994; US-217948.

28 -JUI-1995; US-217948.

24 -MAR-1994; US-217948.

24 -MAR-1994; US-217948.

25 -JUI-1995; US-217948.

26 -JUI-1995; US-217948.

27 -JUI-1995; US-217948.

28 -JUI-1995; US-217948.

29 -JUI-1995; US-217948.

20 -JUI-1995; US-21796.

20 -JUI-1996; US-21796.

20
                                                                                                                                                                                   Varicella zoster virus; VZW; anti-VZW monoclonal antibody; 93KA9;
glycoprotein II subunit; vaccine.
                                                                                           02-OCT-1995 (first entry)
93RA9 anti-Varicella zoster virus antibody heavy chain variable.
                                                                                                                                                                                                                                                                           Key Location/Qualifiers 20.147
Protein 20.147
/label- mature light chain 50.54
Region 50.54
/label= complementarity determining region (CDR)
Region 69.85
T 1
R65019 standard; Protein; 147 AA
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                                                                                    02-0CT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
/label= CDR
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This polypeptide sequence comprises the heavy chain variable region
(VH), HBBI, Obtained by mutagenesis of the VH CDR3 of human
carcinoembryonic antigen (hCEA) specific antibody CEA6 (see
W1981). A claimed specific binding member (A) comprises an hCEA
specific antibody antigen binding Jomain that has a dissociation
constant for hCEA of less than 1 x 10 -8 M, is non-cross-reactive
with human liver cells, and preferentially binds to the A3-B3
cextracellular domain of hCEA and/or to cell-associated hCEA over
hCEA over soluble hCEA. Preferred (A) include pairings of VH and
VI. sequences from CEA1-7 (see W1988-95) obtained by
as well as CEA6 VH and VL variants (see W1988-95) obtained by
mtagenesis or chain shuffling. An example of a claimed pairing
is HBB11 VH with CEA6 VL. (A) is used to detect cells expressing
hCEA, in vivo or in vitro, especially tumour cells for diagnosing
                                                                                                                         61 YAQKFQGRLSITADDSTSTAYMELSSTRSEDTAVYFCAR-VVIDNAIPHIMGYY-FDYWG 118
                                                                                                yaqkfqgrvtisadaststaymelsslrsddtamyycarditapgaaptplnfygmdvwg 138
Specific binding members for human carcinoembryonic antigen - bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.8%; Score 613; DB 23; Length 123; 72.4%; Fred. No. 2.20e-38; arive 10, Mismatches 21; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour marker; lung cancer; breast cancer; colon cancer; adenocarcinoma; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                      07-DEC-1997 (first entry)
CEA-specific antibody CEA6 VH mutant HBBIl sequence.
Carcinoembryonic antigen; CEA; human; antibody; scFv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "complementarity determining region 2" 99 \dots 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "complementarity determining region 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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W19888 standard; Protein; 123 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McCafferty JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31..35
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                                                                                                                                                                                           139 ggttvtvss 147
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                                                                                                                                                                                                                                           119 QGTLVTVSS 127
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60 yaqxfqqrltitadeststaymelsslrsedtavyycarhahayel-yy--yymdvwqqq 115
                                              61 YAQKEQGRISITADDSTSTAYMELSSLRSEDTAVYFCARVVIPNAIPHTMGYYFDYWGGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         attachment of staryl Lex side chairs (see R2442, FT). The additional N-linked glycosylation stres are introduced at locations which impair complement fixing and Fe receptor binding ability. They are preferably located in the CH2 region of the Iq molecule.

Antibodies bearing multiple stalyl-Lex determinants are useful for disrupting undestrable interartions between cells or proteins. Disrupting this interaction has therapeutic applications, for example, in minimising inflammation following tissue injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zs gyjin gsgaedkkpyssyknachatissjaismyrjapgitemajiipiidiatan 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The IgG1, in its mascent form, bears no sialy1-10x side chains. The inventors designed a molecule including several such sites for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibition of cell adhesion mediated through ELAM-1 mol. binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used in treating chronic inflammation, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 481;
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Misc_difference 310
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Pred. No. 3.81e-38;
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                                                                                                                                                                                                                                                                                                                                     Sequence of antibody molécule 1gG1. Antibody; immunoglobulin G1.
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R24442 standard; Protein; 481 AA.
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Local Similarity 71.18;
                                                                                                                                                                                                                                                                                                               (first entry)
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23-NOV-1990; US-618314.
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N-PSDB; Q25443.
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                                                                                                                                                       121 TLVTVSS 127
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This polypeptide sequence comprises the heavy chain variable region (VH), HBB6, obtained by mutagenesis of the VH CDR3 of human cardiomembryonic antigen (hCBA) specific antibody CBR6 (see M198B1). A claimed specific binding member (A) comprises an hCBA specific antibody antigen binding member (A) comprises an hCBA specific antibody antigen binding domain that has a dissociation constant for hCBA of less than 1 x 10 -8 M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 extracellular domain of hCBA and/or to cell-associated hCBA over hCBA over soluble hCBA. Preferred (A) include pairings of VH and VL sequences from CBA1-7 (see W19876-85), or their CDR sequences, as well as CBA6 VH and VL variants (see W19886-95) obtained by mutagenesis or chain shuffling. An example of a claimed pairing is HBB6 VH with CBA6 VL (A) is used to defect cells expressing C hCBA, in vivor or in vitro, especially tumour cells for diagnosing cancer, e.g. adenorationma of the colon, lung or breast.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 64.7%; Score 602; DB 23; Length 123; Local Similarity 71.7%; Pred. No. 1.65e-37; les 91; Conservative 10; Mismatches 22; Indels
                                                                                                                                                                                            Carcinoembryonic antigen; CEA; human; antibody; scfv; tumour marker; lung cancer; breast cancer; colon cancer; adenocarcinoma; diagnosis.
                                                                                                                                                                                 CEA-specific antibody CEA6 VH mutant HBB6 sequence.
                                                                                                                                                                                                                                                                                                                                                              /note= "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                     "complementarity determining region 2" 99..112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "complementarity determining region 3"
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07-DEC-1995; GB-03004,
23-MAY-1996; GB-010824,
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                   .r 4
Wl9889 standard, Protein, 123 AA
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                                                                                                                                                          07-DEC-1997 (first entry)
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Chimeric synthetic.
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09-DEC-1996; G03043.
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97-319779/29
144 gtlvtvss 151
                                      120 GILVIVSS 127
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                                                                                                                                                                                                                                                                                                                                              /label= CDR1
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60 yaqkfqgrltitadeststaymelsslrsedtavyycagcshnyel-yy--yymdvwggg 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           with human liver cells, and preferentially binds to the A3-B3 extracellular domain of hCEA and/or to cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include pairings of VH and VL sequences from CEA1-7 (see W19876-85), or their CDR sequences, as well as CEA6 VH and VL variants (see W19886-95) obtained by mutagenesis or chain shuffling. Examples of claimed pairings are 706D10 VH with 706D12 or CEA6 VL. (A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast.
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Pred. No. 1.98e-37;
10; Mismatches 22; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This polypeptide sequence comprises the heavy chain variable region (VH), To6D10, obtained by mutagenesis of the VH CDR3 of human carcinoembryonic antigen (hCBA)-specific antibody CEA6 (see NH19881). A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 -8 M, is non-cross-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Specific binding members for human carcinoembryonic antigen - bind to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing
                                                                                                              tumour marker; lung cancer, breast cancer; colon cancer,
                                                      07-DEC-1997 (first entry)
CEA-specific antibody CEA6 VH mutant T06D10 sequence.
Carcinoembryonic antigen; CEA; human; antibody; scFv;
                                                                                                                                                                                                                                         /hote= "complementarity determining region 1" Region 80..66
                                                                                                                                                                                                                                                                                               /note= "complementarity determining region 2" Region
                                                                                                                                                                                                                                                                                                                                                        "complementarity determining region 3"
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                                                                                                                                                                                                                                                                                                                                                                                                          09-DEC-1996; G03043.
11-CCT-1996; GB-021295.
07-DEC-1995; GB-02004.
23:MAX-1996, GB-010824.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                        Location/Qualifiers
JT 5
W19886 standard; Protein; 123 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 64.5%;
Best Local Similarity 71.7%;
Matches 91; Conservative
                                                                                                                                  adenocarcinoma; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McCafferty JG,
                                                                                                                                                 Chimeric Homo sapiens;
Chimeric synthetic.
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WFI: 97-319779/29.
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/label= CDR3
                                    W19886;
07-DEC-1997
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Claim 4, Fig la; 128pp; English.

This polypeptide sequence comprises the heavy chain variable region (VH) of human carcinoembryonic antigon (hCEA)-specific antibody CEA. VH (172126-32) and VL (172133-35) gene sequences were obtained for anti-hCEA antibodies CEA1-CEA7 (see W19876-85).

A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant of hCEA of less than 1 x 10 -8 M, is non-cross-reactive with human live hCEA and/or to cell-associated hCEA over hCEA over hCEA and/or to cell-associated hCEA over hCEA over hCEA and/or to cell-associated hCEA over hCEA over hCEA and vL sequences from CEA1-7, or their CDE sequences, as well as CEA6 WH and VL variants, including combinations of CEA6 VH with VL CE regions from CEA6, TOGOG, TOGOG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EVÖLLEGSGAEVKKPGSSVKVSCGVFGDTESRYTIGMERGAFGGGFEWMGNIIPVYNTPN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l qvqlv-qsqaevkkpqssvkvsrkasqqtfsnspinwlrqapqqqlewmqsiipsfqtan 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Specific binding members for human carcinoembryonic antigen - bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 22, Indels 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1233
CEA-specific antibody CEA6 VH sequence.
Carcinoembryonic antigen; CEA; human; antibody; scFv;
tumour marker; lung cancer; breast cancer; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carcinoembryonic antigen; CEA; human; antibody; scFv;
tumour marker; lung cancer; breast cancer; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-DEC-1997 (first entry)
CEA-specific antibody CEA6 VH mutant HBAll sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 400; DB 23,
Pred. No. 2.37e-37;
                                                                                                                                                                                                                    /note= "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                    /note= "complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                  "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McCafferty JG, Osbourn JK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W19887 standard; Protein, 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the colon, lung or breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 71.7%;
Matches 91, Conservative
                                                                                      adenocarcinoma; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adenocarcinoma; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-0CT-1996; GB-021295.
07-DEC-1995; GB-025004.
23-MAY-1996; GB-010824.
                                                                                                                                                                   31..35
                                                                                                                                                                                                                                                    50..66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97-319779/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 tmvtvss 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; T72131
                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                           /label= CDR2
                                                                                                                                                                                                                                                                                                                                                        /label= CDR3
                                                                                                                                                                                          /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                               W09720932-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                        -JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Allen DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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This polypeptide sequence comprises the heavy chain variable region (VH), HBAIL, obtained by mutagenesis of the VH CDR3 of human carcinoembryonic antigen (hEAB)-specific antibody CEAB (secondary) A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10 -8 M, is non-cross rearlive with human liver cells, and preferentially binds to the A3-B3 extracellular domain of hCEA and/or to cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include pairings of VH and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expressing beed, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenocateinoma of the colon, lung or breast
                                                                                                                                                                                                                                                                                                                                                                                                               Specific binding members for human carcinoembryonic antiqen - bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hCEA over soluble hCEA. Preferred (A) include pairings of VH and VL sequences from CEA1-7 (see Wig876-85), of their CLB sequences, as well as CEA6 VH and VL variants (see Wi9876-95) othained by mutagenesis or chain shuffling (A) is used to detect cells.
                                                                                                                                                                                                                                                                                                                                                                                                                              to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells, used for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pp 23; Tendth 123;
                                                                                           //note= "complementarity determining region 1"
70..66
                                                                                                                                                     "complementarity determining region 2" 99..112
                                                                                                                                                                                                                 "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1265 ATOMS
                                                                                                                                                                                                                                                                                                                                                     (CAMB.) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Fig 2; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                          McCafferty JG,
                                                                                                                                                                                                                                                                                                              07-DEC-1995; GR-025004
Chimeric Homo sapiens;
                                                                                                                                                                                                                                                                                                                                 23-MAY-1996; GB-010824
                                                                                                                                                                                                                                                                           09-DEC-1996; G03043.
                  Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                                           97-319779/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 AA;
                                                                                                                                                                                                                                      W09720932-A1.
                                                                                                                                    /label= CDR2
                                                                            /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                      Allen D.T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                  /label=
                                                                                                                    Region
                                                                                                                                                           /note=
                                                                                                                                                                                Region
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60 yaqkfqgrltitadeststaymelsslrsedtavyyca q:anscnrsyyyymdvrqqq 116
                                                                     1 qvqlv-qsgaevkkpgssvkvsckasgqtfsnspinwlrqapqqqlewmqsiipsfqtan 59
                                                                                                1 EVELLEGSGAEVKPF SSVEVSFOVEST FESEVELEMETAFOGGEFWARRETFVYNTER 60
                                          4; Gaps
                                          Indels
                                          Mismatches 18;
                            Pred No 4 10e-37;
                                           14:
            64 18:71.78;
Cuery Match
Best Local Similarity 71 /*,
91; Conservative
                                                                                                                                                                                    117 tmvtvss 123
                                                                                                                                                                                                                121 TLVTVSS 127
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R54796, 18-OCT-1994 (first entry) SpA-reactive 1gM heavy chain clone KAS. SpA domain D; 1g binding region; 1gM; B-cell superantiqen; sAq: superantigen; heavy chain variable region; VH3 restricted antibody; VH; protein-A, KAS, B-limphosyte, vaccine.

29-00T-1993; U10555. 30-00T-1992; US-96936. (REGC.) UNIV CALIFORNIA

Homo sapiens. Wog409818-A.

11-MAY-1994

R54796 standard; peptide; 120 AA.

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(WELL ) WELLCOME FOUND LID.
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                                                                                                                                                                                                                                                                                                                                                                                         A Breat Stricted breath super-antigen vacination antibodies - through B-cell super-antigen vacination Disclosure: Page 78; 130pp; Bandish.

Disclosure: Page 78; 130pp; Bandish.

B-cell superantigen (sAg) is a fragment of SpA D domain that specifically binds the Fab pottion of variable region restricted antibodies. The sAg is used to enhance production of VH, sepecially VH3, restricted Abs. During attempts to identify sAgs, as sequences (R54784-801) of H chains from Ig reactive with mod SpA, and as and DNA sequences (EP4882:15, 24481.55) of VH regions of SpA binders (SbA binders) and desired from combinatorial libraries were determined. IgM protein RAS is derived from the germline configuration of a VH gene
                                                                                                                                                                                                                                                                62 AÇKRYƏRLSITALDSISTAYMELSSLASBUTAVYROARVVIRNAIRHTMƏYYRDYMGQƏT 121
                                                                                                                                                                                                      1 vhlv-gsgaevkkpgssvkvsckasggtfssyaiswvrqapggglewmggiipifggany 59
                                                                                                                                                                                                                         2 VQLLEQSGAEVKKFGSSVKVSCQVFGDTFSRYTIQWLRQAFGQGPEWMGNIIFVYNTPNY 61
                                                                                                                                                                                  6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                       Heavy, light, chain, antibody; D; monoclonal; peripheral; blood; lymphocyte; hepatitis A virus; HAV; sero; positive; patient; murine; B5B3; polyadenylated; cDNA library; human; kappa; L; H.
                                                                                                                                                             Match 62.2%; Score 579; DB 9; Length 120; Local Similarity 67.5%; Pred. No. 1.10e-35; es 85; Conservative 17; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                R21022 standard; Protein; 476 AA.
                                                                                                                                                                                                                                                                                                                                                                     19-MAY-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122..132
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GB-015284.
GB-016594.
                                                                                                                                                                                                                                                                                                                                                                                Antibody D heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 113
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          WPI; 94-167127/20.
                                                                                                                                          120 AA;
                                                                                                                                                                                                                                                                                     115 lvtvss 120
                                                                                                                                                                                                                                                                                                         122 EVTVSS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label= HINGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1991;
23-MAP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
/label= GDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
/label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FR3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= FR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= FR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= CH2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                             Seguence
                                                                                                                                                               Query Match
                                                                                                                                  segment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
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                                                                                                                                                                                                                                                                                                                                                           R31023;
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                                                                                                                                                                                 Matches
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The sequences given in R31023-24 represent the heavy and light chains of Antibody D respectively. Antibody D is a monoclonal antibody which was derived from peripheral blood lymphocytes from a hepatitis A virus (HAV) sero positive patient. Antibody D is closely related in nature to munifody BSB3. Total RNA was isolated from antibody D expressing cells and polydonylated RNA was extracted. Those polyh RNA's were used to prepare a cDNA library which was screened for human Further heavy (H) chains and two positive clones were detected. Sequence 476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 ysqnfqgrvtitadkststahmeltslrsedtavyycatdryrqanfdrarvgw-fdpwg 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           All simulations of variable region gene family restricted antibodies - through B-cell super-antigen vaccination Discolosure; Page 77, 130pp; English.

B-cell superantigen (849) is a fragment of SpA D domain that specifically binds the Fab portion of variable region restricted antibodies. The Sap is used to enhance production of VH, sepecially VH3, restricted Abs. During attempts to identify sAgs, as sequences (R54784-801) of H chains from Ig reactive with mod-SpA, and as and DNA sequences (R54802-16, 02481-56) of VH regions of SpA binders bobtained from combinatorial libraries were determined. IgM protein BOR is derived from the germline configuration of a VH gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 vqlv-qsgaevkkpgssvkvtckasgdtfsssaiswvrqapgeglewmggiipifgtpny 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 gmgvv-gsgaevkkpgssvtvsckasggtfsnyaiswvrgapggglewmggiiplfgtpt 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVĄCLEGSSAEVKKPSSEVKVSCGVPSETPSRYTIGMLPQAPGQGPEWMGNIIPVYNTPN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SpA-reactive igM heavy chain clone BOR.
SpA domain D; 1g binding region; 1gM; B-cell superantigen; sAg;
superantigen; heavy chain variable region; VH3 restricted antibody;
VH; protein-A; BOR; B-lymphocyte; vaccine.
                                                                                           Prodn. of recombinant primate antibodies - useful for treating infections caused by hepatitis A, B and C, herpes, cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 61.7%; Score 574; DB 9; Length 120; Best Local Similarity 69.8%; Pred. No. 2.74e-35; Matches 88; Conservative 15; Mismatches 17, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 576; DB 6;
Pred. No. 1.90e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   л 10
R54795 standard; peptide; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 61.9%;
Best Local Similarity 67.4%;
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAY-1994.
29-OCT-1993; U10555.
30-OCT-1992; US-969936.
(PEGC ) UNIV CALIFORNIA.
Crowe JS, Lewis AP;
WPI; 93-019951/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WFI; 94-167127/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 qgtlvtvss 146
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                                                              N-PSDB; Q35099
                                                                                                                                                                                                             arthritis etc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-OCT-1994
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                                            62 AQKFQGRLSITADDSTSTAYMELSSLRSEDTAVYFCARVVIPNAIRHTMGYYFDYWGQGT 121
2 VOLLEVSGARVKKPGSSVKVSGUVEGFFSBYTTGWLFGARGGSPRWGATTPVYNTPNY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 qvqlv-qsgaevkkpgssvkvsckasgqtfssyaiswvrqapqqqlewmgqiipifgtan 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVÜLLEQSGAEVKKPGSSVKVSCQVFGDTFSRYTIQMLRQAPGQGPEMMGNIIPVYNTPN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                     by molecular cloning of immunoglobulin genes by PCR Disclosure; Page 68; 94pp; English.

L. and H-chain DNA was amplified by PCR from Graves' orbital tissue and clones encoding autoimmune-associated immunoglobulin fragments were obtained. 13/15 clones of H chain [1931] genes showed homology to the closest germline genes, DP10 (089327) and hv1263 (089328). The DNA (089329) and corresp. amino acid (R72070) sequences of the VH region of a representative clone, Sequence 98 AA;
                                                                                                                                                                                                                                                                                                                                                                             Graves' ophthalmopathy-associated monoclonal antibody - produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Humanised 5G1.1 VH + IGHRL.
Complement C5; haemolysis; kidney; glomerulonephritis;
monoclonal antibody: antihofammatory; antibody engineering;
humanised antibody; complementarity determining region; Ole
                                                                                                                                                                                            orbital antigen, monoclonal antibody; heavy chain, H chain, variable region; autoimmunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 572; DB 12; Length 98; Prod No 3,946-35; 11; Mismatches 9; Indels
                                                                                                                                                                                 Graves ophthalmopathy associated immunoglobulin protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 yaqkfqgrvtitadeststaymelsslrsedtavyycar 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 YAQKFQGRESITADDSTSTAYMELSSLRSEDIAVYFOAR 99
                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     22-SEF-1993; US-124469.
(NICH-) NICHOLS INST DIAGNOSTICS.
                                                                                                                                     R72068 standard; Protein; 98 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R77610 standard Protein: 249 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 61.4%;
Best Local Similarity 78 8%;
                                                                                                                                                           26-SEP-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                              Rapoport B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78; Conservative
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/label= sig.peptide
201.249
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                                                                                                                                                                                                                                                                                                            22-SEP-1994; U10756
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WPI: 95-139383/18.
                                                                   115 lvtvss 120
                                                                                         122 LVTVSS 127
                                                                                                                                                                      DP10 VH region.
                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; Q89327
                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                         /label= CDR2
                                                                                                                                                                                                                                                   /label= CDP1
                                                                                                                                                                                                                                                                                                 30-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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Treating glomerulonephritis with antibody against complement C5 component to inhibit complement induced cell lysis Example 11, Fuge 119-122, 181pp. English.

A humanised CDK-grafted and framework sequence-altered Fd, 551.1 VH + IGHPL (P77510), includes CDRs derived from mouse anti-C5 monoclonal antibody 561.1. It can be co-expressed with a humanised light chain (P77512) in human 22* ERNA cells using encoding DNAs subcloned into vector APEX-*P (T08475). Such humanised recombinant antibodies retain the ability of MAP 561.1 to block human complement C5a generation and thus to reduce glomerular inflammation and kidney dysfunction associated with glomerulonephritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Programment the many chains of the human anti-herpes monoclonal antihody clone EachsVW. This antibody is capable of neutralising both herpes simplex virus (HSV) types I and II by binding an epitope present on diveoprotein D. The antibody may be used for detecting HSV in vivo on in vitro; for passive immunotherapy (pref. prophylactically) of HSV infection (eq. genital, oral or coular herpes), partic, as its Fab fragment and as a competitive reagent for detection neutralising anti-HSV antibodies in a sample. Anti-idiotypic antibodies raised against the mAb can be used for active immunotherapy of HSV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 yaqkfqgrytmtadtststaymelsslrsedtavyycaryffgss-pu---wyfdvwqqq 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 gygly-gsgaeykkpgasykysokasgyifsnywigwyrgapggglewmgeilpasaste 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVÖLLEÖSGAEVKKPGSSVKVSCOVFGDTFSPYTTÖWLROAPGOCPEWMGNITPVYNTPN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Gaps
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Disclosure: Page 72: 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human monoclonal antibodies that neutralise Herpes simpley virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PR 14; Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     derpes simplex virus, type I, type II, monoclonal antibody; diagnosis; neutralisation; immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                              Rollins S;
                                                                                                                                                                                                                                                                                                                                           Thomas TC;
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HSV-neutralising antibody clone FabHSV8 heavy chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 572; PR 14;
Pred. No. 3.94e-35;
                                                                                                                                                                                                                                                                                                              Nye SH,
                                                                                                                                                                                                                                                                                                        Evans MJ, Matis L, Mueller EE, Nye SH,
Rother RP, Springhorn J P, Squinto SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R75964 standard; peptide: 122 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.4%;
68.5%;
                                                                                                                                                                                                                                             02-MAY-1994; US-235208.
(ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87; Conservative
                                                                                           118 130
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(SCRI ) SCRIPPS RES INST
                             66..79
                                                                                                                                                                                                                                                                                                                                                                  Wang Y, Wilkins JA;
WPI; 95-392923/50
                                                                                                                                                                                                                      01-MAY-1995; U05688.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sest Local Similarity
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95-254909/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 AA;
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                                                                                                                           /label= CDR-H3
                                                             CDE-HC
/label= CDR-Hl
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                                                                                                                                                            WO9529697-A1.
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                                                                                                                                                                                         09-NOV-1995.
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                                   Region
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                                                                 label
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Search completed: Tue Feb 24 07:06:25 1998
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                                                                                                                                                                                                                                                                          1 legsgaevkkpgssvkvsckasggsfssyainwvrgapggglewmgglmpifgttnyagk 60
                                                                                                                                                                                              5 LEQSGAEVKKPGSSVKVSCQVFGDTFSRYTIQWLPQAPGQGPEWMGNIIPVYNTPNYAQK 64
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                                                                                              1, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          component - to inhibit complement induced cell lysis
Claim 37: Pages 135-137: 181pp: English.
A DNA construct (108487) codes for a humanised CDR-grafted
light chain, designated 5G1.1 VL + IGHRLD (R77615), which includes
CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA can be subcloned together with DNA (T08484) coding for a humanised Fd (R77611) into vector APEX-3P (T08476) for expression of humanised antibody in human 293 EBNA cells. Such recombinant antibodies retain the ability of MAb 561.1 to block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating glomerulonephritis with antibody against complement C5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D.2-APR-1996 (first entry)

Humanised 5G1.1 VH + IGHRLD.

Complement C5: haemolysis: kidney: glomerulonephritis:
monoclonal antibody: antiinflammatory: antibody engineering:
humanised antibody. complementariry determining region: CLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 60.3%; Score 561; DB 14; Length 249; Best Local Similarity 64 94; Pred No. 2.93e-34; Matches 85; Conservative 16; Mismatches 21; Indels 5
                                                 Length 122;
                                            Score 565; DB 14; Length 122
Pred. No. 1.41e-34;
14, Mismatches 26, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mueller EE, Nye SH, Rollins S; rn J P, Squinto SP, Thomas TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T 14
R77515 standard; Protein; 249 AA.
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                                            60.78;
                                                                                                Conservative
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(ALEX-) ALEXION PHARM INC
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                  Ouery Match
Best Local Similarity 6
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Peptide 20..
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01-MAY-1995; U05688.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glomerulonephritis.
Sequence 249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rother RP, Springl
Wang Y, Wilkins JA
WPI, 95-392923/50.
122 AA;
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                                                                                                                                                                                                                                                                                                                                                                                             125 VSS 127
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Evans MJ,
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From a cancer patient

Claim 19: Page 75-76: 82pp; English.

A process for isolating and synthesising human monoclonal anti-tumour
antibodies has been produced. The process involves: (a) constructing at
least one fusion phage library from the peripheral blood lymphocytes

(PBLS) of a cancer patient; (b) screening for anti-tumour antibodies in
the phage library in a binding assay with cultured tumour cells of the
same type as the patient's tumour; (c) removing extraneous antibodies in
the phage library in a binding assay with cultured tumour cells of the
same type as the patient's tumour; (c) removing extraneous antibodies by
absorption against normal human cells; (d) cloning the phage selected in
step (b) and (c); (e) assaying the specificity of the cloned phage by
coubating the phage with at least two types of cultured normal cells;
and (f) further testing the specificity of cloned phage that do not bind
to cultured tumour cells derived from more than one other tumour that is
not the patient's tumour. The present sequence represents a human heavy
chain antibody, from a VH antibody fusion phage library, produced by
a method as described above. The antibodies produced can be used for
diagnostic and therapeutic applications and for isolating tumour

antigens for studying tumouringeness or for use as anti-cancer vaccines.
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                                                                                                                       28-OCT-1997 (first entry)
Anti-melanoma antibody 2-71 from VH antibody fusion phage library.
Human: monoclonal antitumour antibody: peripheral blood lymphocyte;
cancer: tumourigenesis; anticancer vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The human antibodies have low immunogenicity in humans compared to murine monoclonal antibodies (MAbs). Since the antibodies are isola from fusion phage libraries, their affinity and specificity for a tumour cell line can be improved by genetic manipulations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prodn. of human monoclonal anti-tumour antibodies - by screening a fusion phage library produced using peripheral blood lymphocytes
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I 15
W13536 standard; protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                          23-JAN-1997.
28-JUN-1996; IB1032.
30-JUN-1995; US-497647.
(UXYA.) UNIV YALE.
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WPI; 97-109061/10.
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinkurgh, U.F Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn MasPar time 129.01 Seconds 825.290 Million cell updates/sec Tue Feb 24 13:29:24 1998; Run on.

Tabular output not generated.

>US-08-844-215-27 (1-378) from USÖ8844115.seq 378

CTTTTGGTCACGTGTCTTCA 378 GAGACCAGTGGCACAGAAGT CTCCACGTCGACGAGCTCAC. 1 GAGGINGNGCIGCTCSAGIC Description: Perfect Score: N.A. Sequence Comp:

TABLE default Gap 6 Scoring table.

Dhase 3: Query 0 SIL Nmatch 397346 seqs, 141010104 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

EST-C

DST.C. 1. EST197 2. EST198 3 EST199 4 EST109 7 FET101 6 EST102 7 EST103 8 EST104 9 EST104 1 EST109 7 EST103 8 EST104 9 EST104 1 E

Database:

BST-D 99 EST295 100 EST296 161 EST297 192 EST248 193 EST244 104:EST300 105 EST301 106 EST302 107 EST303 108 EST304 1109 EST305 110 EST306 111 EST307 112 EST308 113 EST309 114 EST310 115 EST311 116 EST312 117 EST313 118 EST314 119 EST315

Mean 9.914; Variance 1.852; scale 5 354 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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16-MAY-1997 CDNA SLOGU T V-1 PPSION		hordata; hini; Homi	sel,G., Jo Martin,J., heising,B.
AAPO1381 16-MAY-1997 EST 16-MAY-1997 2744992 II Spains over 1990 HTT H mo sagleds over 2000 705034 St similar to gb/MX8512 IG HEAVY CHAIN FFP07HSOF V-1 FFGION		human. Homo sapiens Erkaryotae, mitechodirisi cokapyotek Metadoa, Chordata; Vertebrata; Mammalia; Eutheria; Primates, Catarrhini; Hominidae; Homo.	1 (bases 1 to 379) HillierL., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schollenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,P. and Wilson,P.
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379 bp Spares Hout, to gb:M18512		s mitorboniti	1 (bases 1 to 379) Hillier,L., Alleb,M., Bowles, Kucaba,T., Lacy,M., Le. N., Le Moore,B., Schellenberg,K., St White,Y., Wylie,T., Waterstor WashU-Merck EST Project 1997
AA201381 0044902.rl	(HUMAN);. AA291381 91939359 EST.	human. Homo sapiens Eskaryetae. : Vertebrata, 1 Homo.	1 (bases 1 to 379) Hillier, L., Allen, M., Kucaba, T., Lacy, M., Moore, B., Schellenbe White, Y., Wylle, T., WashU-Merck EST Proj
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                                                                                                                                                                                                                                                                                                                  EST13661 Testis tumor Homo sapiens cDNA 5' end similar to similar to immunoglobulin mu heavy chain, VDJC regions (GB:M18512).
                                                                                                                                           Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE consortium (info@imaqe.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 361.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                               /note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a modified polylinker, Site_1. Not I; Site_2: Eco RI; Ist
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                                                                                                                                                                                                                                                                                                                                                                                                                             (Pharmacia), Library constructed by Bento Soares and M.Fatima Bonaldo."/Clone="725234"
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Adams.M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
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                                                                                          4444 Forest Park Parkway, Box 8501, St Louis. Mo 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 72; Indels 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="DH10B (ampicillin resistant)"
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Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 132; DB 99;
Pred. No 2 256·221;
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74.5%;
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Matches 216; Conservative
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Unpublished (1997)
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Fax: 314 286 1810
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White, O., Staten G., Riake, S. A., Rrandon, R. C., Man-Wai, C., Clayton, R. A., Chino, T. R., Contron, M. D., Farle-Hudhos, J., Fine, L.D., Fitzgeradd, L.M., Fitzhaman, J.L., Geodhaden, N.S., Glodek A., Gnehm, C.L., Bannan M. C., Hebblom, E., Hinkle, P. S.Jr., Palley, J. M., Felley, I. M., McTeno-Palanques, R.F., McDonald, L.A., Nudyen, D.T., Pelliquino, S.M., Philips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriqqs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Weil, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Pillion, P. J., Fancon, W. P., Rosen, C. M., Haseltine, W. A., Fiolds, C., Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    For clone availability, additional sequence and expression information related to this EST, please check the TIGE Human General and at this LYANAMALISH (ALTD-//ANAMALISH LYANAMALISH) Seq primer: MI3 Reverse.
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Bookl, Site_2: Xbol"
/clone_lib="Testis tumor"
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EST89603 Small intestine I Homo sapiens cDNA 5' end similar to
similar to imminoglobalin heavy chain, Viol regions (GB.214165).
AA377074
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Relt, C.J., Loo, N.H., Kirkboss, F.F., Weinsterk, K.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center trive, Packrille, Mr 20850 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 119; DR 25; Pred. No. 1.73e-193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ______
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<1...279
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O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Other_ESTS: THC166571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.5%;
81.1%;
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Best Local Similarity
Matches 154; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical
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ORGANISM

REFERENCE

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Adams, M.D. Kerlavage, A.R., Fleischmann, P.D., Fuldher, P.A.,
Bult, C.T., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Goragne, T.D.,
Whiten, Sutton, G., Plake, T.A., Brandon, P.C., Man, Wai, C.,
Clayton, P.A., Cline, T.P., Cotton, M.D., Earle-Hughes, T.,
Fitzgerald, L.M., Fitzhugh, W.M., Eritchman, J. I., Geoghagen, N.S.,
Glode, A.A., Gheho, C.E., Hanne, M.A., Fitchman, J. I., Geoghagen, N.S.,
Moreno-Palanques, P.F., McDenald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Pyder, S.E., Scott, J.L., Saudek, M., Shirley, P.,
Small, K.V., Spriggs, T.A., Titerback, T.P., Weidman, T.R., Li, Y.,
Bednarik, D.P., Cao, L., Copeda, M.A., Coleman, T.A., Collins, E.T.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Rozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melsner, P.S., Olsen, H.,
Raymond, L., Weil, Y.F., Wing, T., Xu, C., Yu, G.T., Plank, A.K.,
France, C.M., Ming, T., Xu, C., Yu, G.T., Plank, S.C.,
France, C.M., Ming, T., Xu, C., Yu, G.T., Plank, S.C.,
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France, C.M., Ming, T., Xu, C., Yu, G.T., Realds, C.,
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France, C.M., Ming, T., Xu, C., Yu, G.T., Realdin, C.,
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France, C.M., Ming, T., Xu, C., Yu, G.T., Realds, C.,
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France, C.M., Ming, T., Xu, C., Yu, G.T., Realds, C.,
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France, C.M., Ming, T., Xu, C., Yu, G.T., Realds, C.,
France, C.M., Ming, T., Xu, C., Yu, G.T., Realds, C.,
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France, C.M., Ming, T., Xu, C., Yu, G.T., Realds, C.,
France, C.M., Ming, T., Xu, C., Yu, G.T., Realds, C.,
France, C.M., Ming, T., Xu, C., Yu, G.T., Realds, C.,
France, C.M., Ming, T., Xu, C., Yu, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial assessment of human gone diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: MI3 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: small intestine; Vector: pBluescript SK-; Site_1: EcoR: Site_2: Xho!"
/clone_lib="Small intestine I"
/dcv_stage="adult"
                                                                                                                                                                                                                                                          Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ASSTGCAGGTGCTGGGGTGTGGGGTGTGAGGTGTGAAGAGGTGGGGGTGTGGGTGAAGGTGT 61
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Pred. No. 3.75e-126,
0; Mismatches 34; Indels 0; Gaps
                                                                                                                                                                                   Homo sapiens
Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata,
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similar to immunoglobulin heavy chain, VDJ region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kerlavage, AR
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Best Local Similarity 77.8%;
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                        (bases 1 to 265)
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                                       ACCESSION
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                                                                                                                 KEYWORDS
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                                                                                                                                Tobases 1 to 291)

Adams, M.D., Kerlavage, A.P., Fleischwann, P.D., Fuldner, P.A.,
Bult.C.J., Leen.N.H., Kirkness, E.F., Walistock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, P.A., Cline, T.P., Cotton, M.D., Earla-Hughes, J., Fine, L.D.,
Fliqqerald, L.M., Fitzhugh, W.M., Fritchman, T.L., Googhagen, N.S.,
Glodek, A., Gnehm, C.L., Hannan, M.C., Hadblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Pelanques, R.F., McDonald, L.A., Nuvyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shiley, R.,
Small, K.V., Spriggs, T.A., utterback, T.P., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Bulms, D., Fenrie, A., Fischer, C., Hustings, G.A.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Puben, S.M.,
Dillion, P.J., Fannon, M.R., Posen, C.A., Haseltine, M.A., Fields, C.,
Fraser, C.M., and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www figr org/tdb/hgi/hgi/hgi)
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/clone_lib="Small intestine I"
/dev_stage="adult"
                                   -Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCUS AA377128 265 bp mRNA EST 21-APR-1997 DEFINITION EST89660 Small intestine I Homo sapiens cDNA 5' end similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 gtgcagctggtgcaatctggggctgaggtgaaggagcctgggttcttctgtgaaagtntcg 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 tgcaaggctattggatacacctcactgattatactatcaactgggtgcgacaggccct 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 IGCAGGGCTCTCGGAGGCAGATTCAGAAGCTACAATTCGAGTGGGTGCGACAGGCCCCT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 ggacagggacttgagtggatggatggatggatgaacccagcaaatggaggctccgactgtgca 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 GGACAAGGICTIGAGIGGAIGGGAAGGAATATCCCIAIGIITGGAAACAAAACIACGCA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 GIGCAGCIGCICGAGICIGGGICTGAGGIGAGAGAGCCTGGGICTICGGIGAAGGICTGT 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9712 Medical Center Drive, Pockville, MP 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 53; Indels
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Pred. No 1.85e-176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 cagaagtttcggggggagagtcaccctgaccacggac 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ml3 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 29 4%;
Local Similarity 75.5%;
nes 163; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 3018699423
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       Homo sapiens
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Query Match

Matches

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16-MAY-1997

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RESULT

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zu47h07.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone 741181
5' similar to gb-M97789 1G GAMMA-1 CHAIN C PECTON (HUMAN);
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                                                                                                                                                            Vertebrata; Mammalia; Eutheria; Primates, Catarihini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image llnl.gov) for further information Seq primer: -28ml3 rev2 ET from Amersham.
                                                                                                                                                                                                           Hiller, L. Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, R., White, Y., Wylie, T., Waterston, P., and Wilson, P., Theising, R., Washu-Merck EST Project 1997
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                                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/sex="Female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="ovarian tumor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                         WashU-Merck EST Project
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Best Local Similarity 82.5%;
Matches 99; Conservative
                                                                                                                                                                                              (bases 1 to 266)
                                                                                                                                                                                                                                                                                                           Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                     Homo sapiens
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92056386
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JOURNAL
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                                       ACCESSION
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                                                                                                                                                                                                                   AUTHORS
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

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Adams, M. D., Kerlavage, A. R., Fleischmann, K. D., Fuldner, K. A., Adams, M. D., Kerlavage, A. R., Fleischmann, K. D., Fuldner, K. A., Acasayne, J. D., White, O., Sutton, G. Blake, J. A., Brandon, R. C., Man-Wai, C., Clayton, R. A., Cline, T. R., Cotton, M. D., Earlo-Hudhes, J., Fine, L. D., Flidgerald, L. M., Fifthugh, W. M., Fritchman, J. G. Graddaden, N. S., Glodelm, C. L., Hanna, M. C., Hebliom, E., Hinkle, P. S. Jr., Mcheep-Palanques, E. F., McDenald, L. A., Marmaros, S. M., Merrick, J. M., Kelley, J. C., Lau, L. L., Marmaros, S. M., Merrick, J. M., Phillips, C. A., Pyder, S. E., Scott, J. L., Saudek, D. L., Pelligrino, S. M., Phillips, C. A., Pyder, S. E., Scott, J. L., Marmaros, S. M., Merrick, D. P., Cao, L., Cepeda, M. A., Crleman, T. A., Collins, E. J., Phillips, C. A., Pyder, S. E., Ferrie, A., Fierher, C. Hastings, G. A., Hey, W. W., Hu, J. S., Greene, J. M., Gruber, J. Hastings, G. A., Kozak, D. L., Kunsch, C., Hungjun, J., Li, H., Meissner, P. S., Olsen, H., Raymond, L., Well, Y., Wing, J., Xu, C., Yu, G., Yu, G., Lille, W. A., Fields, C., Fraser, C.M. and Venter, J., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J. C. (2007), 3-174 (1995)
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5' similar to qt-M87789 15 GAMMA-1 CHAIN C MEGION (HUMAN);.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Generalets (http://www.tigr.org/tdb/hdi/hgi.html)
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Eukaryotae: mitochendrial eukaryotes: Metazoa: Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae:
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: thymus: Vector: pBluescript SK-; Site_1:
EcoR; Site_2: XhoI"
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9712 Medical Center Drive, Rockville, Mp 20850 USA
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larity 76.2%; Pred No. 6 23e-66;
Conservative 6, Mismatches 25;
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<1..>198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Kerlavage, AR
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Best Local Similarity
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Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J. (Lee, N. H., Kirkness, E.F., Weinstock, K.G., Gorayne, J.D.,
White, O., Sutton, G., Blake, J.A.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Eatle-Hughes, G.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, F., Hinkle, P.S.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.E., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.
Small, K.V., Spriggs, T.A., Collins, E.J.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
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//organism="Homo sapiens"
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                  Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy M., Le. N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R., and Wilson, P., Markers, E. T. Project 1997.
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Vertebrata, Mammalia, Eutheria, Frimates; Catarthini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -26ml3 rev2 ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-1997
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EST69374 Lymph node I Homo sapiens cDNA 5' end similar to
immunoglobulin heavy chain, VDJ regions (GB·X67906)
AA360195
                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine 4444 Forest Park Parkway, Rox 8501, St. Louis, MC 63108 Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares ovary tumor NbHOT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="ovarian tumor"
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                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="Female"
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Best Local Similarity 92.5%;
Matches 49; Conservative
1 (bases 1 to 230)
Hillier,L., Allen.M
Kucaba,T., Lacy.M.,
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                                                                                                                                                                                                                                                            Unpublished (1997)
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                                                                                                                                                                                                                       TITLE
         REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                              COMMENT
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/note="Organ: lymph node; Vector: pBluescript SR·; Site_l:
CooRi: Site_2: Xhol"
/Clone_lib="Lymph node I"
/dev_stage="adult"
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Adams. M.D. Kerlavage. A.R. Fleischmann, R.D., Fuldner, R.A.,
White, S. G., Googane, J.D.,
White, S. Stiton, H., Ritkness, F. W. Man. Wal. C.,
Clayton, R.A., Cline, T.P., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Flizgerald, L.M., Fitchugh, W.M., Fricchman, J.L., Googhagen, N.S.,
Glock, A., Gochm. C.L., Hanna, M.C., Hedblom, E.B., Hinkle, F.S. Jr.,
Kelley, J.M., Kelley, T., Hanna, M.C., Hedblom, E.M., Merrick, J.M.,
Phillips, C.A., Ryder, S.E., Sectt, J.L., Squdek, D.M., Shirley, R.,
Small, K.V., Sprigges, T.A., Utterback, T.R., Weiddman, J.E., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
                                                                                                                                                  Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
He,W W, Hi,J S , Greene,J.M , Gruber,J., Hudson,P , Kim,A K ,
Kozak,D.I., Kunsch,C . Hungjun,J , Li,H , Mei*sner,P.S., Olsen,H.,
Baymond,L., Wei,Y P., Wing,J., Xu,C , Yu,G L., Ruben,S.M.,
Dillion,P J., Fannon,M. F , Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C M and Venter,J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Generalor (http://www.tigr.crg/tdt/hgi.html)
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 cetgeactgtetetggtgtetecgteagtaattaetagtagagetggateegacagteee 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 11.5%; Score 44; DB 52; Longth 258; Best Local Similarity 64.8%; Pred, No. 1.56e-41; Matches 94; Conservative 0; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        9712 Medical Center Prive, Pockwille, MD 20850 USA
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The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 CIGGACAAGGICITGAGIGGAIGGG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seg primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                 Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                             Other_ESTs: THC169164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 3018699423
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                                                                                                                                                                                                                      JOURNAL
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl): 3-174 (1995)
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gorayne, T.D.,
White, O., Sutton, G., Rlake, J.A., Frandon, B.C., Man Wai, C.,
Clayton, R.A., Cilne, T.E., Cotton, M.D., Earle-Hughes, J., Finc, L.D.,
Fitzgerald, L.M., Fitzhugh, M.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblow, E., Hinkle, P.S.Jr.,
Kelley, J.M., Kelley, J.C., Lill, T.L., Marmanca, S.M., Merrick, J.M.,
Morero-Palanques, R.F., Monopald, L.A., Manyon, P., Polligrin, S.M.,
Phillips, C.A., Ryder, S.F., Scott, J.L., Saudek, D.M., Shirloy, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi html)
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,T., Li,H., Moissner,P.S., Olsen,H.
Raymond,L., Weit,Y.F., Wing,J.T.,Xu,C., Yu,G.L., Puben,S.M.
Dillion,P.J., Fennon,M.R., Posen,G.A., Hassitine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
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ECORI; Site_2: XhoI"
/clone_lib="Testis tumor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TCCTGCAGGGGCTGTGGAGGGAGATTGAGAATTTGAATTGAATTGGGGTGGGAGAGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 gaggigeagaigitiggagingggggggggnilggianageniggggggieeniganaeic 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 tectgigeagtetetgggtteaeetttagegaetaegeeatgagetgggteegeeagget 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAGGIGCACCIGCICGAGICTGAGGICTGAGGAGGAGGAGGICTGGGTGAAGGIC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similar to immunoglobulin mu heavy chain, V region. AA295703
                                                                                                                                                                                                                                                                                                                                                                                                       The Institute for Genomic Research 9712 Medical Conter Drive, Rockville, MD 20850 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Socation/Qualifiers
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<1..>273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                             Other_ESTs: THC179200
Contact: Kerlavage, AP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3018699056
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LOCUS AA3CC289 243 bp mENA incl 21-APR-1997
DEFINITION EST69410 Tymph node, subtracted Home sapiens cDNA 5 end similar to
Small.K.V. Spriqas,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Dimke,D., Penq.D.-F., Ferda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Fenq.D.-F., Ferrica,A., Fischer,C., Hastinas,G.A., Hay,W.W., Hu, IS. Grone,I.W., Striber, I. Hidsen, P. Kim A.K., Kozak,D.L., Kunsch,C., Hundjun,J., Li,H., Meissner, P.S., Olsen,H., Raymond,L., Wei,Y.F., Wind,J., Xu,C., Yu,G.I., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Frasex,C.M. and Venter,J.C.
Initial assessment of human gone diversity and expression patterns Initial assessment of human gone diversity and expression patterns based upon 83 million nucleotides of cDNA sequence.
Nature 377 (6547 Suppl.), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          For clone availability, additional sequence and expression information related to this EST, please check the TIGE Human General Index (http://www.tigr.org/tdb/hai/hqi.html)
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EcoRE: Site_2: XhoI"
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White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae, mitochondria) eukaryotes, Metazoa, Chordata.
Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 GSTGCSACAGSCCCTGSACAAGSTCTTSAGTGGCAAGAATCATCCCTATGTTCGC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 ABTABCABABTAGGGAGABABELLICABBBAGAGAGAGAATTAGGGGGGAAGAATTGAA 227
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1 Homes 1 to 240)
Adams.M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldmer,R.A.,
Adams.M.D., Kerlavage,A.R., Fleischmann,R.D., Gulayme,
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(GB:003894).
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Pred. No. 1.01e<sup>23</sup>9;
0: Mismatches 71: Indels
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The Institute for Genomic Research
9712 Medical Center Prive, Rockville, Mp 20850 USA
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/dev_stage="adult"
<1..>341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                     Contact: Kerlavage, AR
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11.4%;
Best Local Similarity 61.0%;
Matches 111; Conservative
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RESULT 13
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Clayton, P.A., Cline, T.F., Cotton, M.D., Earle-Hughes, T., Fine, L.D., Fitzerald, E.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Geneho, C.L., Banna, M.C., Heddlome, E., Hinkle, P. F., F., Kelley, J.G., Hanna, M.C., Heddlome, E., Hinkle, P. F., Kelley, J.G., Liu, L.-T., Marmarcs, S.M., Merrick, J.M., Moreno-Palanques, F.F., McDenald, L.A., Nuyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D. M., Shirley, F., Small, K.V., Spriggs, T.A., Utterback, T.F., Weldman, L.F., Y., Bednarik, D.P., Cac, L., Cepeda, M.A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Caene, J.M., Gruber, J., Huston, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melssner, P.S., Olsen, H., Paymond, L., Wal, Y.F., Wing, J., Xu, C., Yu, G.L., Puhen, S.M., Pillion, P.J., Fannon, M.P., Fannon, M.
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/note="Organ: lymph node. Vector. pBluescript SK+; Site_1.
ECOPI: Site_2* Xho!"
/dclone_lib="Lymph node, subtracted"
/clone_lib="Lymph node, subtracted"
/li>240
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, T.D.,
White, O., Sutton, G., Blake, J.A., Brandon B.C., Man-Wai, C.
Clayton, R.A., Gline, T.P., Cothron, D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhop, W.M., Fritchman, T.L., Georhagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkie, P.S. Tr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     For clone availability, additional sequence and expression information related to this EST, please check the IIGR Human Gene Index (http://www.tigr.org/tdb/hqi/hqi.html)
Seq primer: M13 Reverse.
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Vertebrata, Mammalia, Butheria, Primates, Catarrhini, Hominidae,
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Pred. No. 1.29e-32,
0, Mismatches 39, Indels 0, Gaps
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9712 Medical Center Drive, Pockville, MP 20950 USA
Tel: 3018699056
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Best Local Similarity 66.7%;
Matches 78; Conservative
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Eclicy, J. M. Kelloy, J.C., Hall. - I., Marmaros, S.M., Morrero-Palanques, R.F., McDonald, L.A., Nuyen, D.T., Pelliarino, S.M., Phillips, C. A., Pyder, S.E., Kertel, T. I., Saudek, D. M., Shirley, R., Small, K.C., A., Utterthack, T. R., Weddman, T.F., Hi, Y., Pigner, D., Pengla, M. A., Coleman, T. A., Collins, E.J., Dirke, D., Pengla, D., Greeda, M. A., Coleman, T. A., Collins, E.J., Pirke, D., F. Fertie, A., Fischer, C., Hastings, G.A., He, W. M., Hu, J.S., Green, J. M., Gruber, J. Meissnet, P.S., Olsen, H., Raymond, J., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Puben, S.M., Phillion, P.J., Pannor, M. P. Posen, G.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                             Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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Seq primer: MI3 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Eukaryotae, mitochondilal eukaryotes, Metazoa, Chordata:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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Best Local Similarity 63.9%: Pred. No. 7.078-31;
Matches 85: Conservative 0: Mismatches 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Other_ESTs: THC167575
Contact: Kerlavage, AR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 3018699423
Email: arkerlav
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Glodek, A. Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Mornor-Balanques, R.F., McChald, L.A., Nquyen, D.T., Pelliarino, S.M., Phillips, C.A., Byder, S.E., Scott, J.L., Saudek, D.M., Shirley, P. Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J.F., Li, Y. Dimke, D.F., Cach, C., Cepeda, M.A., Coleman, T.F., Collins, E.J., Dimke, D., Feng, D.-F., Ferrick, A. Fisher, C., Hastings, G.A., He, W., Hu, S., Greene, J.M., Gruber, T. Hudson, P. Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Palymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M. P. Posen, C.A., Haseltine, W.A., Fields, C. Fraser, C.M., and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                   Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, R.G., Cocayno, T.D.,
White, O., Sutton, G., Rlake, J.A., Rrandon, P.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi html) Seq primer: M13 Reverse
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Vertebrata; Mammalla; Eutherla; Primates; Catarrhini: Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 tectgigeagectetggatteattiteaacagitaeageatgaaeigggieegeeageie 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9712 Medical Center Drive, Pockville, MD 20850 USA
Tel: 3018699056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: arkerlav@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Kerlavage, AR
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Alloydes, A. Grebber, C. L. Hanna, M. C. Hoddlom, E. Hinklo, P. S.Jr. Kelley, T. M. Kelley, T. C. Liu, L. J. Marmaros, S.M., Morrick, J.M., Marmaros, S.M., Morrick, J. M., Shillips, G. R., Strath, T. L., Sandrk, D.M., Shilley, R. Small, K.V., Spriggs, T.A., Utterback, T.R., Woldman, J.F., Li, Y. Bednarik, D.P., Gao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D. Y., Ferrisa, A. Fishber, G. Hastinds, G. H., Kozak, D.L., Kunsch, C., Hundjun, J., Li, H., Meissner, P.S., Olsen, H., Paymond, L., Weily, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Pallino, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Flelds, G., Fraser, C.M., and Venter, J.C.
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Bult, C. I., Toe, N. H., Kirkness, F. F., Weinsteck, V. G., Greayme, J.D.,
White, O., Sutton, G., Elake, J.A., Frandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hudhes, J., Fine, L.D.,
Flizgerald, L.M., Fitzhudh, W.M., Fritchman, J.L., Groqhaqen, N.S.,
Glodek, A., Gnohm, C.L., Hanna, M.C., Hedbjon, E., Hinkley, R.S., Y.
Kelley, J.M., Kelley, J.C., Liu, L.T., Marmaros, S.M., Merrick, J.M.,
McCreno, Palanques, R.P., McConald, L.A., Mauyen, D.T., Polliarino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION EST94138 Activated T-cells XII Homo sapions cum 5, and similar to similar to immunoclobulin mu heavy chain, V region. Agg1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Initial assessment of human gene diversity and expression patterns based upon 83 million nucleofides of cDNA sequence
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Pritchman, 11, Geoghaden, N.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Si... Propis Site_2:
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordala;
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/dev_stage="adult, 20 yrs"
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Pred. No. 9.49e·26;
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Fitzhugh, W.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: arkerlav@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.98;
Matches 40; Conservative
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Fitzgerald, L. M.
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Small.K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li.Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Bednarik,D.P., Feng,D.-F., Fercher,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P. Kim.A.K., Kozak,D. L., Kunsch,C., Hungjun, T., Li,H., Meissner,P.S., Olsen,H., Kaymond,L., Wei,Y.F., Wing, Y. Xu,C., Yu,G. L., Ruben,S.M., Dillion,P.J., Fennen,M. F., Puseu,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence
Nature 377 (6547 Suppl.), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi html) Seq primer: MI3 Reverse
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/note="Vector pRluescript SK+, Site_1 EreRI; Site_2
XhoI"
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
TTEL: 3018699056
Fax: 3018699423
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/cell_type="T-iymphocyte"
/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                               Contact: Kerlavage, AR
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Local Similarity 60.7%;
les 88; Conservative
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96
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COMMENT
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